

REC'D 08 DEC 2000

WIPO

PCT

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

(PCT Article 36 and Rule 70)

Applicant's or agent's file reference SCB/50899026	FOR FURTHER ACTION	See Notification of Transmittal of International Preliminary Examination Report (Form PCT/IPEA/416)
International application No. PCT/EP99/05991	International filing date (day/month/year) 16/08/1999	Priority date (day/month/year) 14/08/1998
International Patent Classification (IPC) or national classification and IPC C12N15/31		
Applicant JANSSEN PHARMACEUTICA N.V. et al.		

1. This international preliminary examination report has been prepared by this International Preliminary Examining Authority and is transmitted to the applicant according to Article 36.



2. This REPORT consists of a total of 6 sheets, including this cover sheet.

- ☐ This report is also accompanied by ANNEXES, i.e. sheets of the description, claims and/or drawings which have been amended and are the basis for this report and/or sheets containing rectifications made before this Authority (see Rule 70.16 and Section 607 of the Administrative Instructions under the PCT).

These annexes consist of a total of sheets.

3. This report contains indications relating to the following items:

- I ☒ Basis of the report
- II ☐ Priority
- III ☒ Non-establishment of opinion with regard to novelty, inventive step and industrial applicability
- IV ☒ Lack of unity of invention
- V ☒ Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement
- VI ☐ Certain documents cited
- VII ☐ Certain defects in the international application
- VIII ☒ Certain observations on the international application

Date of submission of the demand 23/02/2000	Date of completion of this report 05.12.2000
Name and mailing address of the international preliminary examining authority:  European Patent Office D-80298 Munich Tel. +49 89 2399 - 0 Tx: 523656 epmu d Fax: +49 89 2399 - 4465	Authorized officer Marinoni, J-C Telephone No. +49 89 2399 8563 

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

International application No. PCT/EP99/05991

I. Basis of the report

1. This report has been drawn on the basis of *(substitute sheets which have been furnished to the receiving Office in response to an invitation under Article 14 are referred to in this report as "originally filed" and are not annexed to the report since they do not contain amendments (Rules 70.16 and 70.17).):*

Description, pages:

1-54 as originally filed

Claims, No.:

1-40 as originally filed

Drawings, sheets:

1/64-64/64 as originally filed

2. With regard to the **language**, all the elements marked above were available or furnished to this Authority in the language in which the international application was filed, unless otherwise indicated under this item.

These elements were available or furnished to this Authority in the following language: , which is:

- ☐ the language of a translation furnished for the purposes of the international search (under Rule 23.1(b)).
- ☐ the language of publication of the international application (under Rule 48.3(b)).
- ☐ the language of a translation furnished for the purposes of international preliminary examination (under Rule 55.2 and/or 55.3).

3. With regard to any **nucleotide and/or amino acid sequence** disclosed in the international application, the international preliminary examination was carried out on the basis of the sequence listing:

- ☐ contained in the international application in written form.
- ☐ filed together with the international application in computer readable form.
- ☐ furnished subsequently to this Authority in written form.
- ☐ furnished subsequently to this Authority in computer readable form.
- ☐ The statement that the subsequently furnished written sequence listing does not go beyond the disclosure in the international application as filed has been furnished.
- ☐ The statement that the information recorded in computer readable form is identical to the written sequence listing has been furnished.

4. The amendments have resulted in the cancellation of:

- ☐ the description, pages:
- ☐ the claims, Nos.:

**INTERNATIONAL PRELIMINARY
EXAMINATION REPORT**

International application No. PCT/EP99/05991

☐ the drawings, sheets:

5. ☐ This report has been established as if (some of) the amendments had not been made, since they have been considered to go beyond the disclosure as filed (Rule 70.2(c)):

(Any replacement sheet containing such amendments must be referred to under item 1 and annexed to this report.)

6. Additional observations, if necessary:

III. Non-establishment of opinion with regard to novelty, inventive step and industrial applicability

The questions whether the claimed invention appears to be novel, to involve an inventive step (to be non-obvious), or to be industrially applicable have not been examined in respect of:

- ☐ the entire international application.
- ☒ claims Nos. 3, 13, 25-33, 36, 37, 40 completely; 1, 2, 4-12, 4-24, 34, 35, 38, 39 partially.

because:

- ☐ the said international application, or the said claims Nos. relate to the following subject matter which does not require an international preliminary examination (*specify*):
- ☐ the description, claims or drawings (*indicate particular elements below*) or said claims Nos. are so unclear that no meaningful opinion could be formed (*specify*):
- ☐ the claims, or said claims Nos. are so inadequately supported by the description that no meaningful opinion could be formed.
- ☒ no international search report has been established for the said claims Nos. 3, 13, 25-33, 36, 37, 40 completely; 1, 2, 4-12, 4-24, 34, 35, 38, 39 partially.

2. A meaningful international preliminary examination report cannot be carried out due to the failure of the nucleotide and/or amino acid sequence listing to comply with the standard provided for in Annex C of the Administrative Instructions:

- ☐ the written form has not been furnished or does not comply with the standard.
- ☐ the computer readable form has not been furnished or does not comply with the standard.

IV. Lack of unity of invention

1. In response to the invitation to restrict or pay additional fees the applicant has:

- ☐ restricted the claims.

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

International application No. PCT/EP99/05991

- ☐ paid additional fees.
- ☐ paid additional fees under protest.
- ☒ neither restricted nor paid additional fees.
2. ☐ This Authority found that the requirement of unity of invention is not complied and chose, according to Rule 68.1, not to invite the applicant to restrict or pay additional fees.
3. This Authority considers that the requirement of unity of invention in accordance with Rules 13.1, 13.2 and 13.3 is
- ☐ complied with.
- ☒ not complied with for the following reasons:
see separate sheet
4. Consequently, the following parts of the international application were the subject of international preliminary examination in establishing this report:
- ☐ all parts.
- ☒ the parts relating to claims Nos. 1, 2, 4-12, 4-24, 34, 35, 38, 39.

V. Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement

1. Statement

Novelty (N)	Yes:	Claims	1, 2, 4-8, 11, 12, 14-24, 34, 38, 39
	No:	Claims	9, 10, 35
Inventive step (IS)	Yes:	Claims	1, 2, 4-8, 11, 12, 14-24, 34, 38, 39
	No:	Claims	9, 10, 35
Industrial applicability (IA)	Yes:	Claims	1, 2, 4-11, 12, 14-24, 34, 35, 38, 39
	No:	Claims	NONE

2. Citations and explanations **see separate sheet**

VIII. Certain observations on the international application

The following observations on the clarity of the claims, description, and drawings or on the question whether the claims are fully supported by the description, are made:
see separate sheet.

Re Item IV

Lack of unity of invention

An objection for lack of unity of the invention was raised by the International Search Authority. No additional search fees were paid. Consequently, the present examination is restricted to group 1 of identified inventions, *i.e.* nucleic acid molecules comprising SEQ ID No:1, polypeptide of SEQ ID No:43 and related topics (antibodies, pharmaceutical compositions, etc...), subject-matter of **claims 1, 2, 4-8, 11, 12, 14-24, 34, 38, 39** partially.

Re Item V

Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement

Reference is made to the following document:

D1: MOLEC. MICROBIOL., Vol. 16, No. 1, 1995, pages 157-167, Reifenberger et al.
'Identification of novel HXT genes in *Saccharomyces cerevisiae* reveals the impact of individual hexose transporters on glycolytic flux'

1. The subject-matter of **claims 1, 2, 4-8, 11, 12, 14-24, 34, 38, 39** related to the nucleic acids of SEQ ID No. 1 or the polypeptide of SEQ ID No. 43 is neither disclosed or suggested in the available prior art.
Therefore, this specific subject-matter meets the requirement of Article 33(2) PCT concerning novelty and the requirements of Article 33(3) concerning inventive step.
2. **D1** discloses a gene which shares 69.5% identity over an 1457 bp overlap with the nucleic acid sequence of SEQ ID No. 1. It is considered that the homology is such that the complementary strand of the sequence of **D1** hybridizes to the SEQ ID No. 1 even under stringent conditions.
Therefore, the subject-matter of **claims 9 and 10** does not meet the requirements of Article 33(2) PCT concerning novelty.
3. Additionally, the sequence disclosed in **D1** contains some stretches of 10-50 nucleotides which are identical to the oligonucleotides of **claim 35**.
Therefore, the subject-matter of **claim 35** does not meet the requirements of

**INTERNATIONAL PRELIMINARY
EXAMINATION REPORT - SEPARATE SHEET**

International application No. PCT/EP99/05991

Article 33(2) PCT concerning novelty.

Re Item VIII

Certain observations on the international application

The wording of **claim 24** can be construed as comprising methods of identifying unspecified compounds which modulate the expression of unspecified polypeptides in *C. albicans* cells having or not a mutation in the nucleic acid sequence of SEQ ID No. 1. The subject-matter of **claim 24** would then be not sufficiently clear nor disclosed (Articles 5 and 6 PCT).

PATENT COOPERATION TREATY

PCT

INTERNATIONAL SEARCH REPORT

(PCT Article 18 and Rules 43 and 44)

Applicant's or agent's file reference SCB/50899026	FOR FURTHER ACTION <small>see Notification of Transmittal of International Search Report (Form PCT/ISA/220) as well as, where applicable, item 5 below.</small>	
International application No. PCT/EP 99/ 05991	International filing date (day/month/year) 16/08/1999	(Earliest) Priority Date (day/month/year) 14/08/1998
Applicant JANSSEN PHARMACEUTICA N.V. et al.		

This International Search Report has been prepared by this International Searching Authority and is transmitted to the applicant according to Article 18. A copy is being transmitted to the International Bureau.

This International Search Report consists of a total of 6 sheets.

☐ It is also accompanied by a copy of each prior art document cited in this report.

1. Basis of the report

- a. With regard to the **language**, the international search was carried out on the basis of the international application in the language in which it was filed, unless otherwise indicated under this item.

☐ the international search was carried out on the basis of a translation of the international application furnished to this Authority (Rule 23.1(b)).

- b. With regard to any **nucleotide and/or amino acid sequence** disclosed in the international application, the international search was carried out on the basis of the sequence listing :

☒ contained in the international application in written form.

☒ filed together with the international application in computer readable form.

☐ furnished subsequently to this Authority in written form.

☐ furnished subsequently to this Authority in computer readable form.

☐ the statement that the subsequently furnished written sequence listing does not go beyond the disclosure in the international application as filed has been furnished.

☐ the statement that the information recorded in computer readable form is identical to the written sequence listing has been furnished

2. ☒ **Certain claims were found unsearchable** (See Box I).

3. ☒ **Unity of invention is lacking** (see Box II).

4. With regard to the **title**,

☒ the text is approved as submitted by the applicant.

☐ the text has been established by this Authority to read as follows:

5. With regard to the **abstract**,

☒ the text is approved as submitted by the applicant.

☐ the text has been established, according to Rule 38.2(b), by this Authority as it appears in Box III. The applicant may, within one month from the date of mailing of this international search report, submit comments to this Authority.

6. The figure of the **drawings** to be published with the abstract is Figure No. _____

☐ as suggested by the applicant.

☐ because the applicant failed to suggest a figure.

☐ because this figure better characterizes the invention.

☐ None of the figures.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/EP 99/05991

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.: 25-28
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

See additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1, 2, 4-12, 14-28, 34, 35, 38, 39 all partially

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Invention 1: claims 1,2,4-12,14-28,34,35,38,39,
all partially

Nucleic acid molecule comprising seq.ID.1 or capable of hybridizing thereto, polypeptide of seq.ID.43 encoded by said nucleic acid, expression vector comprising said nucleic acid, antibody against said peptide, use of said vector for preparation of medicament or pharmaceutical composition, C. albicans cell comprising an induced mutation in said DNA sequence, oligonucleotides comprising 10-50 nt of said nucleic acid sequence, and method for identifying compounds which modulate expression of said nucleic acid.

2. Inventions 2-68: claims 1,6-11,15-28,34,35,38,
39 partially, and 2-5,12-14,36,37,
40 partially as applicable

As invention 1, but limited to the respective nucleic acid sequences 2,3,5,10,11,12,16,17,18,20,21,23,25,26,27,29,31,33,35,37,39,41,44,45,46,49,50,52,55,57,59,61,63,65,67,70,72,74,76,78,80,81,83,85,87,89,91,93,95,97,99,101,104,106,108,110 and 113, and polypeptide sequences corresponding to said nucleic acid sequences in as far as they are provided (see table 1 of the description), whereby invention 2 is limited to seq.ID.2, invention 3 is limited to seq.ID.3 and its translated polypeptide seq.ID.4,, and invention 68 is limited to seq.ID.113 and its translated polypeptide sequence seq.ID.114.

In as far as a polypeptide sequence, translated from the ORF of a corresponding nucleic acid sequence is provided, the polypeptide encoded by the corresponding nucleic acid sequence and their use in the preparation of a medicament, and antibodies against said polypeptide is also considered part of the respective invention.

3. Invention 69: claim 29-33

Method for identifying DNA sequences from a cell or organism, which encode polypeptides which are critical for growth and survival for said cell or organism, comprising screening a library of nucleic acids using a vector that either integrates into the genome of said cell or organism, or that permits expression of antisense RNA, and selecting growth-impaired cells or organisms. Plasmids pGAL1PSiST-1 and pGAL1PNiST-1, used in said method.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 25-28

Claims 25-28 refer to a compound identifiable with a method, without giving a true technical characterization of the compound. Moreover, no such compounds are defined in the application. In consequence, the scope of said claims is ambiguous and vague, and their subject-matter is not sufficiently disclosed and supported (Art. 83 and 84 EPC).

No search can be carried out for such purely speculative claims whose wording is, in fact, a mere recitation of the results to be achieved.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

INTERNATIONAL SEARCH REPORT

International Application No

T/EP 99/05991

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/31 C07K14/40 A61K31/70 A61K38/16 C07K16/14
G01N33/50 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K A61K G01N C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	REIFENBERGER E ET AL: "IDENTIFICATION OF NOVEL HXT GENES IN SACCHAROMYCES CEREVISIAE REVEALS THE IMPACT OF INDIVIDUAL HEXOSE TRANSPORTERS ON GLYCOLYTIC FLUX" MOLECULAR MICROBIOLOGY, GB, OXFORD, vol. 16, no. 1, 1 January 1995 (1995-01-01), pages 157-167, XP000572126	9, 10, 35
A	the whole document	23
A	EP 0 844 307 A (SMITHKLINE BEECHAM CORP) 27 May 1998 (1998-05-27) the whole document	24, 38, 39
	--- -/--	

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

1 February 2000

Date of mailing of the international search report

27.04.00

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

Authorized officer

Smalt, R

INTERNATIONAL SEARCH REPORT

International Application No

EP 99/05991

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	DALY S ET AL: "Isolation and characterization of a gene encoding alpha-tubulin from Candida albicans" GENE: AN INTERNATIONAL JOURNAL ON GENES AND GENOMES,GB,ELSEVIER SCIENCE PUBLISHERS, BARKING, vol. 187, no. 2, 7 April 1997 (1997-04-07), page 151-158 XP004093273 ISSN: 0378-1119 the whole document ---	
A	WO 97 36925 A (SCRIPTGEN PHARM INC ;HARVARD COLLEGE (US)) 9 October 1997 (1997-10-09) the whole document ---	
A	WO 97 37230 A (BRADLEY JOHN;WOBBE C RICHARD; BURATOWSKI STEPHEN) 9 October 1997 (1997-10-09) the whole document ---	
A	WO 96 36707 A (UNIV ROMA ;IST SUPERIORE SANITA (IT); CASSONE ANTONIO (IT); VALLE) 21 November 1996 (1996-11-21) the whole document -----	

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

EP 99/05991

Patent document cited in search report		Publication date	Patent family member(s)		Publication date
EP 0844307	A	27-05-1998	US	5869290 A	09-02-1999
			CA	2216616 A	21-05-1998
			JP	10201490 A	04-08-1998

WO 9736925	A	09-10-1997	CA	2250129 A	09-10-1997
			EP	0904289 A	31-03-1999

WO 9737230	A	09-10-1997	US	5863762 A	26-01-1999
			CA	2250121 A	09-10-1997
			EP	0894269 A	03-02-1999

WO 9636707	A	21-11-1996	IT	RM950314 A	18-11-1996
			AU	5777696 A	29-11-1996
			EP	0826040 A	04-03-1998

PATENT COOPERATION TREATY

PCT

NOTIFICATION OF ELECTION

(PCT Rule 61.2)

From the INTERNATIONAL BUREAU

To:

Assistant Commissioner for Patents
United States Patent and Trademark
Office
Box PCT
Washington, D.C.20231
ETATS-UNIS D'AMERIQUE

in its capacity as elected Office

Date of mailing (day/month/year)
30 March 2000 (30.03.00)

International application No.
PCT/EP99/05991

Applicant's or agent's file reference
SCB/50899026

International filing date (day/month/year)
16 August 1999 (16.08.99)

Priority date (day/month/year)
14 August 1998 (14.08.98)

Applicant

CONTRERAS, Roland, Henri et al

1. The designated Office is hereby notified of its election made:

☒ in the demand filed with the International Preliminary Examining Authority on:
23 February 2000 (23.02.00)

☐ in a notice effecting later election filed with the International Bureau on:

2. The election ☒ was
☐ was not

made before the expiration of 19 months from the priority date or, where Rule 32 applies, within the time limit under Rule 32.2(b).

The International Bureau of WIPO
34, chemin des Colombettes
1211 Geneva 20, Switzerland

Facsimile No.: (41-22) 740.14.35

Authorized officer

Claudio Borton

Telephone No.: (41-22) 338.83.38

PATENT COOPERATION TREATY

PCT

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

(PCT Article 36 and Rule 70)

Applicant's or agent's file reference SCB/50899026	FOR FURTHER ACTION		See Notification of Transmittal of International Preliminary Examination Report (Form PCT/IPEA/416)
International application No. PCT/EP99/05991	International filing date (day/month/year) 16/08/1999	Priority date (day/month/year) 14/08/1998	
International Patent Classification (IPC) or national classification and IPC C12N15/31			
Applicant JANSSEN PHARMACEUTICA N.V. et al.			
<p>1. This international preliminary examination report has been prepared by this International Preliminary Examining Authority and is transmitted to the applicant according to Article 36.</p> <p>2. This REPORT consists of a total of 6 sheets, including this cover sheet.</p> <p><input type="checkbox"/> This report is also accompanied by ANNEXES, i.e. sheets of the description, claims and/or drawings which have been amended and are the basis for this report and/or sheets containing rectifications made before this Authority (see Rule 70.16 and Section 607 of the Administrative Instructions under the PCT).</p> <p>These annexes consist of a total of sheets.</p>			
<p>3. This report contains indications relating to the following items:</p> <ul style="list-style-type: none"> I <input checked="" type="checkbox"/> Basis of the report II <input type="checkbox"/> Priority III <input checked="" type="checkbox"/> Non-establishment of opinion with regard to novelty, inventive step and industrial applicability IV <input checked="" type="checkbox"/> Lack of unity of invention V <input checked="" type="checkbox"/> Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement VI <input type="checkbox"/> Certain documents cited VII <input type="checkbox"/> Certain defects in the international application VIII <input checked="" type="checkbox"/> Certain observations on the international application 			
Date of submission of the demand 23/02/2000		Date of completion of this report 05.12.2000	
Name and mailing address of the international preliminary examining authority: <div style="display: flex; align-items: center;"> <div> European Patent Office D-80298 Munich Tel. +49 89 2399 - 0 Tx: 523656 epmu d Fax: +49 89 2399 - 4465 </div> </div>		Authorized officer Marinoni, J-C Telephone No. +49 89 2399 8563	



**INTERNATIONAL PRELIMINARY
EXAMINATION REPORT**

International application No. PCT/EP99/05991

I. Basis of the report

1. This report has been drawn on the basis of *(substitute sheets which have been furnished to the receiving Office in response to an invitation under Article 14 are referred to in this report as "originally filed" and are not annexed to the report since they do not contain amendments (Rules 70.16 and 70.17).):*

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1-40 as originally filed

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1/64-64/64 as originally filed

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These elements were available or furnished to this Authority in the following language: , which is:

- ☐ the language of a translation furnished for the purposes of the international search (under Rule 23.1(b)).
- ☐ the language of publication of the international application (under Rule 48.3(b)).
- ☐ the language of a translation furnished for the purposes of international preliminary examination (under Rule 55.2 and/or 55.3).

3. With regard to any **nucleotide and/or amino acid sequence** disclosed in the international application, the international preliminary examination was carried out on the basis of the sequence listing:

- ☐ contained in the international application in written form.
- ☐ filed together with the international application in computer readable form.
- ☐ furnished subsequently to this Authority in written form.
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4. The amendments have resulted in the cancellation of:

- ☐ the description, pages:
- ☐ the claims, Nos.:

**INTERNATIONAL PRELIMINARY
EXAMINATION REPORT**

International application No. PCT/EP99/05991

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(Any replacement sheet containing such amendments must be referred to under item 1 and annexed to this report.)

6. Additional observations, if necessary:

III. Non-establishment of opinion with regard to novelty, inventive step and industrial applicability

The questions whether the claimed invention appears to be novel, to involve an inventive step (to be non-obvious), or to be industrially applicable have not been examined in respect of:

☐ the entire international application.

☒ claims Nos. 3, 13, 25-33, 36, 37, 40 completely; 1, 2, 4-12, 4-24, 34, 35, 38, 39 partially.

because:

☐ the said international application, or the said claims Nos. relate to the following subject matter which does not require an international preliminary examination (*specify*):

☐ the description, claims or drawings (*indicate particular elements below*) or said claims Nos. are so unclear that no meaningful opinion could be formed (*specify*):

☐ the claims, or said claims Nos. are so inadequately supported by the description that no meaningful opinion could be formed.

☒ no international search report has been established for the said claims Nos. 3, 13, 25-33, 36, 37, 40 completely; 1, 2, 4-12, 4-24, 34, 35, 38, 39 partially.

2. A meaningful international preliminary examination report cannot be carried out due to the failure of the nucleotide and/or amino acid sequence listing to comply with the standard provided for in Annex C of the Administrative Instructions:

☐ the written form has not been furnished or does not comply with the standard.

☐ the computer readable form has not been furnished or does not comply with the standard.

IV. Lack of unity of invention

1. In response to the invitation to restrict or pay additional fees the applicant has:

☐ restricted the claims.

**INTERNATIONAL PRELIMINARY
EXAMINATION REPORT**

International application No. PCT/EP99/05991

- ☐ paid additional fees.
- ☐ paid additional fees under protest.
- ☒ neither restricted nor paid additional fees.
2. ☐ This Authority found that the requirement of unity of invention is not complied and chose, according to Rule 68.1, not to invite the applicant to restrict or pay additional fees.
3. This Authority considers that the requirement of unity of invention in accordance with Rules 13.1, 13.2 and 13.3 is
- ☐ complied with.
- ☒ not complied with for the following reasons:
see separate sheet
4. Consequently, the following parts of the international application were the subject of international preliminary examination in establishing this report:
- ☐ all parts.
- ☒ the parts relating to claims Nos. 1, 2, 4-12, 4-24, 34, 35, 38, 39.

V. Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement

1. Statement

Novelty (N)	Yes:	Claims	1, 2, 4-8, 11, 12, 14-24, 34, 38, 39
	No:	Claims	9, 10, 35
Inventive step (IS)	Yes:	Claims	1, 2, 4-8, 11, 12, 14-24, 34, 38, 39
	No:	Claims	9, 10, 35
Industrial applicability (IA)	Yes:	Claims	1, 2, 4-11, 12, 14-24, 34, 35, 38, 39
	No:	Claims	NONE

2. Citations and explanations
see separate sheet

VIII. Certain observations on the international application

The following observations on the clarity of the claims, description, and drawings or on the question whether the claims are fully supported by the description, are made:
see separate sheet

Re Item IV

Lack of unity of invention

An objection for lack of unity of the invention was raised by the International Search Authority. No additional search fees were paid. Consequently, the present examination is restricted to group 1 of identified inventions, *i.e.* nucleic acid molecules comprising SEQ ID No:1, polypeptide of SEQ ID No:43 and related topics (antibodies, pharmaceutical compositions, etc...), subject-matter of **claims 1, 2, 4-8, 11, 12, 14-24, 34, 38, 39** partially.

Re Item V

Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement

Reference is made to the following document:

D1: MOLEC. MICROBIOL., Vol. 16, No. 1, 1995, pages 157-167, Reifenger et al.
'Identification of novel HXT genes in *Saccharomyces cerevisiae* reveals the impact of individual hexose transporters on glycolytic flux'

1. The subject-matter of **claims 1, 2, 4-8, 11, 12, 14-24, 34, 38, 39** related to the nucleic acids of SEQ ID No. 1 or the polypeptide of SEQ ID No. 43 is neither disclosed or suggested in the available prior art.
Therefore, this specific subject-matter meets the requirement of Article 33(2) PCT concerning novelty and the requirements of Article 33(3) concerning inventive step.
2. **D1** discloses a gene which shares 69.5% identity over an 1457 bp overlap with the nucleic acid sequence of SEQ ID No. 1. It is considered that the homology is such that the complementary strand of the sequence of **D1** hybridizes to the SEQ ID No. 1 even under stringent conditions.
Therefore, the subject-matter of **claims 9 and 10** does not meet the requirements of Article 33(2) PCT concerning novelty.
3. Additionally, the sequence disclosed in **D1** contains some stretches of 10-50 nucleotides which are identical to the oligonucleotides of **claim 35**.
Therefore, the subject-matter of **claim 35** does not meet the requirements of

Article 33(2) PCT concerning novelty.

Re Item VIII

Certain observations on the international application

The wording of **claim 24** can be construed as comprising methods of identifying unspecified compounds which modulate the expression of unspecified polypeptides in *C. albicans* cells having or not a mutation in the nucleic acid sequence of SEQ ID No. 1. The subject-matter of **claim 24** would then be not sufficiently clear nor disclosed (Articles 5 and 6 PCT).

PATENT COOPERATION TREATY

From the INTERNATIONAL BUREAU

To:

BOULT WADE TENNANT
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**INFORMATION CONCERNING ELECTED
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(PCT Rule 61.3)

Date of mailing (day/month/year) 30 March 2000 (30.03.00)		
Applicant's or agent's file reference SCB/50899026		IMPORTANT INFORMATION
International application No. PCT/EP99/05991	International filing date (day/month/year) 16 August 1999 (16.08.99)	
		Priority date (day/month/year) 14 August 1998 (14.08.98)
Applicant JANSSEN PHARMACEUTICA N.V. et al		

1. The applicant is hereby informed that the International Bureau has, according to Article 31(7), notified each of the following Offices of its election:

AP : GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW

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2. The following Offices have waived the requirement for the notification of their election; the notification will be sent to them by the International Bureau only upon their request:

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TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW

3. The applicant is reminded that he must enter the "national phase" before the expiration of 30 months from the priority date before each of the Offices listed above. This must be done by paying the national fee(s) and furnishing, if prescribed, a translation of the international application (Article 39(1)(a)), as well as, where applicable, by furnishing a translation of any annexes of the international preliminary examination report (Article 36(3)(b) and Rule 74.1).

Some offices have fixed time limits expiring later than the above-mentioned time limit. For detailed information about the applicable time limits and the acts to be performed upon entry into the national phase before a particular Office, see Volume II of the PCT Applicant's Guide.

The entry into the European regional phase is postponed until 31 months from the priority date for all States designated for the purposes of obtaining a European patent.

The International Bureau of WIPO
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Authorized officer:

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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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(21) International Application Number: PCT/EP99/05991 (22) International Filing Date: 16 August 1999 (16.08.99) (30) Priority Data: 9817796.7 14 August 1998 (14.08.98) GB 98310694.9 23 December 1998 (23.12.98) EP (71) Applicant (for all designated States except US): JANSSEN PHARMACEUTICA N.V. [BE/BE]; Turnhoutseweg 30, B-2340 Beerse (BE). (72) Inventors; and (75) Inventors/Applicants (for US only): CONTRERAS, Roland, Henri [BE/BE]; University of Gent, K.L. Ledeganckstraat 35, B-9000 Gent (BE). NELISSEN, Bart [BE/BE]; Janssen Pharmaceutica N.V., Turnhoutseweg 30, B-2340 Beerse (BE). DE BACKER, Marianne, Denise [BE/BE]; Janssen Pharmaceutica N.V., Turnhoutseweg 30, B-2340 Beerse (BE). LUYTEN, Walter, Herman, Maria, Louis [BE/BE]; Janssen Pharmaceutica N.V., Turnhoutseweg 30, B-2340 Beerse (BE). VIAENE, Jasmine, Elza [BE/BE]; University of Gent, K.L. Ledeganckstraat 35, B-9000 Gent (BE). LOGGHE, Marc, George [BE/BE]; University of Gent, K.L. Ledeganckstraat 35, B-9000 Gent (BE).	(74) Agent: BOULT WADE TENNANT; 27 Furnival Street, London EC4A 1PQ (GB). (81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 22 June 2000 (22.06.00)	
(54) Title: DRUG TARGETS IN CANDIDA ALBICANS		
(57) Abstract <p>The present invention is concerned with a method of identifying compounds which selectively modulate expression of polypeptides which are crucial for growth and survival of <i>Candida albicans</i>, which method comprises: (a) contacting a compound to be tested with one or more <i>Candida albicans</i> cells having a mutation in a nucleic acid molecule corresponding to the sequences according to any of claims 1 to 8 which mutation results in overexpression or underexpression of said polypeptides, in addition to contacting one or more wild type <i>Candida albicans</i> cells with said compound, (b) monitoring the growth and/or activity of said mutated cell compared to said wild type; wherein differential growth or activity of said one or more mutated <i>Candida</i> cells is indicative of selective action of said compound on a polypeptide or another polypeptide in the same or a parallel pathway. Also disclosed in the present invention are compounds identified and the sequences themselves which are critical for survival and growth of <i>Candida albicans</i>.</p>		

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DRUG TARGETS IN CANDIDA ALBICANS

The present invention is concerned with the identification of genes or functional fragments thereof from *Candida albicans* which are critical for growth and cell division and which genes may be used as selective drug targets to treat *Candida albicans* associated infections. Novel nucleic acid sequences from *Candida albicans* are also provided and which encode the polypeptides which are critical for growth of *Candida albicans*.

Opportunistic infections in immunocompromised hosts represent an increasingly common cause of mortality and morbidity. *Candida* species are among the most commonly identified fungal pathogens associated with such opportunistic infections, with *Candida albicans* being the most common species. Such fungal infections are thus problematical in, for example, AIDS populations in addition to normal healthy women where *Candida albicans* yeasts represent the most common cause of vulvovaginitis.

Although compounds do exist for treating such disorders, such as for example, amphotericin, these drugs are generally limited in their treatment because of their toxicity and side effects. Therefore, there exists a need for new compounds which may be used to treat *Candida* associated infections in addition to compounds which are selective in their action against *Candida albicans*.

Classical approaches for identifying anti-fungal compounds have relied almost exclusively on inhibition of fungal or yeast growth as an endpoint. Libraries of natural products, semi-synthetic, or synthetic chemicals are screened for their ability to kill or arrest growth of the target pathogen or a related nonpathogenic model organism. These tests are

- 2 -

cumbersome and provide no information about a compounds mechanism of action. The promising lead compounds that emerge from such screens must then be tested for possible host-toxicity and detailed mechanism of action studies must subsequently be conducted to identify the affected molecular target.

The present inventors have now identified a range of nucleic acid sequences from *Candida albicans* which encode polypeptides which are critical for its survival and growth. These sequences represent novel targets which can be incorporated into an assay to selectively identify compounds capable of inhibiting expression of such polypeptides and their potential use in alleviating diseases or conditions associates with *Candida albicans* infection.

Therefore, according to a first aspect of the invention there is provided a nucleic acid molecule encoding a polypeptide which is critical for survival and growth of the yeast *Candida albicans* and which nucleic acid molecule comprises any of the sequences of nucleotides in Sequence ID Numbers 1, 2, 3, 5, 10, 11, 12, 14, 16, 18, 20, 21, 23, 25, 27, 29, 31, 33, 37, 39, 41, 44, 45, 46, 49, 50, 52, 55, 57, 59, 61, 63, 65, 67, 70, 72, 74, 76, 78, 80, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 104, 106, 108, 110 and 113, or the sequences of nucleotides identified in Figures 9 to 13.

Whilst the molecules defined herein have been established as being critical for growth and metabolism of *Candida albicans*, for some of the molecules no apparent functionality has been assigned by virtue of the fact that no functionally related sequences in other prokaryotic or eukaryotic organism can be found in respective databases. Thus, advantageously these sequences may be species specific in which case they may be used as selective targets for treatment of diseases mediated by *Candida*

- 3 -

Albicans infection. Thus, in one aspect of the invention the nucleic acid molecules preferably comprise the sequences identified in sequence ID Nos 1, 2, 3, 5, 10, 11, 12, 14, 16, 17, 18, 46, 49, 50, 52, 55, 57, 59, 61, 63, 65, 87, 89, 91, 93, 95, 97, 99, 101, 104, 106, 108, and 110 and the corresponding polypeptide sequences identified in Table 1.

Some of sequences according to invention have been assigned a particular function. Nucleic acid molecules according to this aspect of the invention comprise any of the sequences as described in sequence ID Nos, 20, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 45, 65, 70, 72, 74, 76, 78, 80, 81, 83, 85 and 113 and the corresponding polypeptides identified in Table 1

Letters utilised in the nucleic acid sequences according to the invention to represent the genetic code and which are not recognisable as letters of the genetic code signify a position in the nucleic acid sequence where one or more of bases A, G, C or T can occupy the nucleotide position. Representative ambiguity codes used to identify the range of bases which can be used are as follows:

25	M:	A or C
	R:	A or G
	W:	A or T
	S:	C or G
	Y:	C or T
30	K:	G or T
	V:	A or C or G
	H:	A or C or T
	D:	A or G or T
	B:	C or G or T
35	N:	G or A or T or C

In one embodiment of the above identified aspects

- 4 -

of the invention the nucleic acid may comprise a mRNA molecule or alternatively a DNA and preferably a cDNA molecule.

5 Also provided by the present invention is a nucleic acid molecule capable of hybridising to the nucleic acid molecules according to the invention under high stringency conditions, such as for example, an antisense molecule.

10 Stringency of hybridisation as used herein refers to conditions under which polynucleic acids are stable. The stability of hybrids is reflected in the melting temperature (T_m) of the hybrids. T_m can be approximated by the formula:

15
$$81.5^{\circ}\text{C} + 16.6 (\log_{10}[\text{Na}^+] + 0.41 (\% \text{G\&C}) - 6001/l$$

wherein l is the length of the hybrids in nucleotides. T_m decreases approximately by 1-1.5°C with every 1% decrease in sequence homology.

20 The nucleic acid capable of hybridising to nucleic acid molecules according to the invention will generally be at least 70%, preferably at least 80 or 90% and more preferably at least 95 to 97% homologous to the nucleotide sequences according to the
25 invention.

The DNA molecules according to the invention may, advantageously, be included in a suitable expression vector to express polypeptides encoded therefrom in a suitable host.

30 The present invention also comprises within its scope proteins or polypeptides encoded by the nucleic acid molecules according to the invention or a functional equivalent, derivative or bioprecursor thereof.

35 Therefore, according to a further aspect of the invention there is provided a polypeptide which is critical for the growth and survival of *Candida*

- 5 -

albicans comprising an amino acid sequence of any of Sequence ID Numbers 4, 6 to 9, 13, 15, 19, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 43, 47, 48, 51, 53, 54, 56, 58, 60, 62, 64, 66, 68, 69, 71, 73, 75, 77, 79, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 103, 105, 107, 109, 111, 112, 114 or the sequences illiustrated in Figures 14 or 15.

An expression vector according to the invention includes a vector having a nucleic acid according to the invention operably linked to regulatory sequences, such as promoter regions, that are capable of effecting expression of said DNA fragments. The term "operably linked" refers to a juxta position wherein the components described are in a relationship permitting them to function in their intended manner. Such vectors may be transformed into a suitable host cell to provide for expression of a polypeptide according to the invention. Thus, in a further aspect, the invention provides a process for preparing polypeptides according to the invention which comprises cultivating a host cell, transformed or transfected with an expression vector as described above under conditions to provide for expression by the vector of a coding sequence encoding the polypeptides, and recovering the expressed polypeptides.

The vectors may be, for example, plasmid, virus or phage vectors provided with an origin of replication, optionally a promoter for the expression of said nucleotide and optionally a regulator of the promoter. The vectors may contain one or more selectable markers, such as, for example, ampicillin resistance.

Polynucleotides according to the invention may be inserted into the vectors described in an antisense orientation in order to provide for the production of antisense RNA. Antisense RNA or other antisense

- 6 -

nucleic acids may be produced by synthetic means.

In accordance with the present invention, a defined nucleic acid includes not only the identical nucleic acid but also any minor base variations including in particular, substitutions in bases which result in a synonymous codon (a different codon specifying the same amino acid residue) due to the degenerate code in conservative amino acid substitutions. The term "nucleic acid sequence" also includes the complementary sequence to any single stranded sequence given regarding base variations.

The present invention also advantageously provides nucleic acid sequences of at least approximately 10 contiguous nucleotides of a nucleic acid according to the invention and preferably from 10 to 50 nucleotides. These sequences may, advantageously be used as probes or primers to initiate replication, or the like. Such nucleic acid sequences may be produced according to techniques well known in the art, such as by recombinant or synthetic means. They may also be used in diagnostic kits or the like for detecting the presence of a nucleic acid according to the invention. These tests generally comprise contacting the probe with the sample under hybridising conditions and detecting for the presence of any duplex or triplex formation between the probe and any nucleic acid in the sample.

According to the present invention these probes may be anchored to a solid support. Preferably, they are present on an array so that multiple probes can simultaneously hybridize to a single biological sample. The probes can be spotted onto the array or synthesised *in situ* on the array. (See Lockhart et al., Nature Biotechnology, vol. 14, December 1996 "Expression monitoring by hybridisation to high density oligonucleotide arrays". A single array can contain more than 100, 500 or even 1,000 different

- 7 -

probes in discrete locations.

Advantageously, the nucleic acid sequences, according to the invention may be produced using such recombinant or synthetic means, such as for example, using PCR cloning mechanisms which generally involve making a pair of primers, which may be from approximately 10 to 50 nucleotides to a region of the gene which is desired to be cloned, bringing the primers into contact with mRNA, cDNA, or genomic DNA from a human cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified region or fragment and recovering the amplified DNA. Generally, such techniques as defined herein are well known in the art, such as described in Sambrook et al (Molecular Cloning: a Laboratory Manual, 1989).

The nucleic acids or oligonucleotides according to the invention may carry a revealing label. Suitable labels include radioisotopes such as ^{32}P or ^{35}S , enzyme labels or other protein labels such as biotin or fluorescent markers. such labels may be added to the nucleic acids or oligonucleotides of the invention and may be detected using known techniques per se.

The polypeptide or protein according to the invention includes all possible amino acid variants encoded by the nucleic acid molecule according to the invention including a polypeptide encoded by said molecule and having conservative amino acid changes. Polypeptides according to the invention further include variants of such sequences, including naturally occurring allelic variants which are substantially homologous to said polypeptides. In this context, substantial homology is regarded as a sequence which has at least 70%, preferably 80 or 90% amino acid homology with the polypeptides encoded by

- 8 -

the nucleic acid molecules according to the invention.

A nucleic acid which is particularly advantageous is one comprising the sequences of nucleotides according to Seq ID Nos 1 and 91 in which are specific
5 to *Candida albicans* with no functionally related sequences in other prokaryotic or eukaryotic organism as yet identified from the respective genomic databases.

Nucleotide sequences according to the invention
10 are particularly advantageous for selective therapeutic targets for treating *Candida albicans* associated infections. For example, an antisense nucleic acid capable of binding to the nucleic acid sequences according to the invention may be used to
15 selectively inhibit expression of the corresponding polypeptides, leading to impaired growth of the *Candida albicans* with reductions of associated illnesses or diseases.

The nucleic acid molecule or the polypeptide
20 according to the invention may be used as a medicament, or in the preparation of a medicament, for treating diseases or conditions associated with *Candida albicans* infection.

Advantageously, the nucleic acid molecule or the
25 polypeptide according to the invention may be provided in a pharmaceutical composition together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

Antibodies to the protein or polypeptide of the
30 present invention may, advantageously, be prepared by techniques which are known in the art. For example, polyclonal antibodies may be prepared by inoculating a host animal, such as a mouse, with the polypeptide according to the invention or an epitope thereof and
35 recovering immune serum. Monoclonal antibodies may be prepared according to known techniques such as described by Kohler R. and Milstein C., Nature

- 9 -

(1975)256, 495-497.

Antibodies according to the invention may also be used in a method of detecting for the presence of a polypeptide according to the invention, which method
5 comprises reacting the antibody with a sample and identifying any protein bound to said antibody. A kit may also be provided for performing said method which comprises an antibody according to the invention and means for reacting the antibody with said sample.

10 Proteins which interact with the polypeptide of the invention may be identified by investigating protein-protein interactions using the two-hybrid vector system first proposed by Chien et al (1991).

This technique is based on functional
15 reconstitution *in vivo* of a transcription factor which activates a reporter gene. More particularly the technique comprises providing an appropriate host cell with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription
20 factor having a DNA binding domain and an activating domain, expressing in the host cell a first hybrid DNA sequence encoding a first fusion of a fragment or all of a nucleic acid sequence according to the invention and either said DNA binding domain or said activating
25 domain of the transcription factor, expressing in the host at least one second hybrid DNA sequence, such as a library or the like, encoding putative binding proteins to be investigated together with the DNA binding or activating domain of the transcription
30 factor which is not incorporated in the first fusion; detecting any binding of the proteins to be investigated with a protein according to the invention by detecting for the presence of any reporter gene product in the host cell; optionally isolating second
35 hybrid DNA sequences encoding the binding protein.

An example of such a technique utilises the GAL4

- 10 -

protein in yeast. GAL4 is a transcriptional activator of galactose metabolism in yeast and has a separate domain for binding to activators upstream of the galactose metabolising genes as well as a protein binding domain. Nucleotide vectors may be constructed, one of which comprises the nucleotide residues encoding the DNA binding domain of GAL4. These binding domain residues may be fused to a known protein encoding sequence, such as for example the nucleic acids according to the invention. The other vector comprises the residues encoding the protein binding domain of GAL4. These residues are fused to residues encoding a test protein. Any interaction between polypeptides encoded by the nucleic acid according to the invention and the protein to be tested leads to transcriptional activation of a reporter molecule in a GAL-4 transcription deficient yeast cell into which the vectors have been transformed. Preferably, a reporter molecule such as β -galactosidase is activated upon restoration of transcription of the yeast galactose metabolism genes.

Further provided by the present invention is one or more *Candida albicans* cells comprising an induced mutation in the DNA sequence encoding the polypeptide according to the invention.

A further aspect of the invention provides a method of identifying compounds which selectively inhibit or interfere with the expression, or the functionality of polypeptides expressed from the nucleotides sequences according to the invention or the metabolic pathways in which these polypeptides are involved and which are critical for growth and survival of *Candida albicans*, which method comprises (a) contacting a compound to be tested with one or more *Candida albicans* cells having a mutation in a nucleic acid molecule according to the invention which mutation results in overexpression or underexpression

- 11 -

of said polypeptides in addition to one or more wild type *Candida* cells, (b) monitoring the growth and/or activity of said mutated cell compared to said wild type wherein differential growth or activity of said one or more mutated *Candida* cells provides an indication of selective action of said compound on said polypeptide or another polypeptide in the same or a parallel pathway.

Compounds identifiable or identified using the method according to the invention, may advantageously be used as a medicament, or in the preparation of a medicament to treat diseases or conditions associated with *Candida albicans* infection. These compounds may also advantageously be included in a pharmaceutical composition together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

A further aspect of the invention provides a method of identifying DNA sequences from a cell or organism which DNA encodes polypeptides which are critical for growth or survival, which method comprises (a) preparing a cDNA or genomic library from said cell or organism in a suitable expression vector which vector is such that it can either integrate into the genome in said cell or that it permits transcription of antisense RNA from the nucleotide sequences in said cDNA or genomic library, (b) selecting transformants exhibiting impaired growth and determining the nucleotide sequence of the cDNA or genomic sequence from the library included in the vector from said transformant. Preferably, the cell or organism may be any yeast or filamentous fungi, such as for example, *Saccharomyces cerevisiae*, *Saccharomyces pombe* or *Candida albicans*.

A further aspect of the invention provides a pharmaceutical composition comprising a compound according to the invention together with a

- 12 -

pharmaceutically acceptable carrier, diluent or excipient therefor.

The present invention may be more clearly understood with reference to the accompanying example,
5 which is purely exemplary, with reference to the accompanying drawings wherein:

Figure 1: is an illustration of A)
10 Intergration of the antisense library plasmid (here shown as a linear fragment) at a site (eg. *GAL1* promoter region) within the genome which is non-homologous to the insert DNA. As a result the
15 *GAL1p* region is duplicated and antisense RNA can be formed from GENE X upon induction of *GAL1p*, and B) Intergration due to homologous recombination of the
20 gene insert (GENE X) of an antisense library clone (here shown as a linear fragment) with the homologous gene (gene x) within the *Candida* genome. As a
25 result this gene is duplicated. The first copy of the gene gene X, is flanked by upstream its endogenous promoter and downstream, oppositely-oriented,
30 the *GAL1* promoter resulting in a so-called "collision construct". Antisense RNA can be formed from GENE X upon induction of *GAL1p*. The second copy of the gene, Gene X, is devoid of a promoter and
35 will not be transcribed.

- 13 -

Figure 2: is an illustration of the vectors used for the preparation of a cDNA antisense library, pGALLPNiST-1, (left) and a genomic library, pGALLPNiST-1 (right).

Figure 3: Growth curves in S-glucose and S-galactose medium of respectively the wild type CAI-4 strain and two transformants (clone 36 and 38) showing antisense induced reduction in growth and overall impaired growth, respectively. Growth curves in S-glucose+maltose and S-galactose+maltose medium of respectively the wild type CAI-4 strain and transformants resulting from antisense library transformation.

Figure 4: is an illustration of promoter activity of the *C. albicans* *GAL1* promoter in the absence and presence of maltose as a carbon source.

Figures 5: is a Northern blot analysis of *C. albicans* mRNA in wild type and clone 36 using a *SAM2* and a *TEF3* specific probe.

Figures 6: is A) a Northern blot analysis of sequences of *C. albicans* mRNA in wild type and clone 38 using a *RNR1* and an *ACT1* specific probe; and B) Real Time Quantitative PCR

- 14 -

on *C. albicans* mRNA in wild type and clone 38 using a *RNR1* and *ACT1* specific fluorogenic probe.

5

Figure 7: is a nucleotide sequence of plasmid pGAL1PNiST-1.

10

Figure 8: is a nucleotide sequence of plasmid pGAL1PSiST-1.

15

Figure 9: is a nucleotide sequence of clone 38 which has been assigned *RNR1* functionally.

20

Figure 10: is a nucleotide sequence of clone 113g4.

Figure 11: is a nucleotide sequence of clone 207g4

Figure 12: is a nucleotide sequence of clone 66g4.

25

Figure 13: is a nucleotide sequence of clone 36 which has been assigned *Sam2* functionally.

30

Figure 14: is an amino acid sequence of clone 38.

Figure 15: is an amino acid sequence of clone 36.

35

- 15 -

Figures 16 to 70 are growth curves of *Candida albicans* showing antisense induced reduction in growth by inhibition of molecules according to the invention.

Example

Identification of novel drug targets in *C. albicans* by anti-sense and disruptive integration

The principle of the approach is based on the fact that when a particular *C. albicans* mRNA is inhibited by producing the complementary anti-sense RNA, the corresponding protein will decrease. If this protein is critical for growth or survival, the cell producing the anti-sense RNA will grow more slowly or will die.

Since anti-sense inhibition occurs at mRNA level, the gene copy number is irrelevant, thus allowing applications of the strategy even in diploid organisms.

Anti-sense RNA is endogenously produced from an integrative or episomal plasmid with an inducible promoter; induction of the promoter leads to the production of a RNA encoded by the insert of the plasmid. This insert will differ from one plasmid to another in the library. The inserts will be derived from genomic DNA fragments or from cDNA to cover-to the extent possible- the entire genome.

The vector is a proprietary vector allowing integration by homologous recombination at either the homologous insert or promoter sequence in the *Candida* genome. After introducing plasmids from cDNA or genomic libraries into *C. albicans*, transformants are screened for impaired growth after promoter (& thus anti-sense) induction in the presence of lithium acetate. Lithium acetate prolongs the G1 phase and

- 16 -

thus allows anti-sense to act during a prolonged period of time during the cell cycle. Transformants which show impaired growth in both induced and non-induced media, thus showing a growth defect due to integrative disruption, are selected as well.

Transformants showing impaired growth are supposed to contain plasmids which product anti-sense RNA or mRNAs critical for growth or survival. Growth is monitored by measuring growth-curves over a period of time in a device (Bioscreen Analyzer, Labsystems) which allows simultaneous measurement of growth-curves of 200 transformants.

Subsequently plasmids can be recovered from the transformants and the sequence of their inserts determined, thus revealing which mRNA they inhibit. In order to be able to recover the genomic or cDNA insert which has integrated into the Candida genome, genomic DNA is isolated, cut with an enzyme which cuts only once into the library vector (and estimated approx. every 4096 bp in the genome) and relegated. PCR with primers flanking in the insert will yield (Partial) genomic or cDNA inserts as PCR fragments which can directly be sequenced. This PCR analysis (on ligation reaction) will also show us how many integrations occurred. Alternatively the ligation reaction is transformed to E. coli and PCR analysis is performed on colonies or on plasmid DNA derived thereof.

This method is employed for a genome wide search for novel C. albicans genes which are important for growth or survival.

MATERIALS AND METHODS

Construction of pGal1NIST-1

pGAL1PNiST-1 (integrative antisense SfiI-NotI vector)

- 17 -

was constructed as described by Logghe et al.,
submitted.

Construction of pGAL1PSiST-1

5

The vector pGAL1PSiST-1 (integrative SfiI-SfiI vector) was created for cloning the small genomic DNA fragments behind the GAL1 promoter. The only difference with pGAL1PNiST-1 is that the hIFNb insert
10 fragment in pGAL1PSiST-1 is flanked by two SfiI sites instead of a SfiI and a NotI site as in pGAL1PNiST-1. To construct pGAL1PSiST-1 the EcoRI-HindIII fragment, containing hIFNb flanked by a SfiI and a NotI site, of pMAL2pHiET-3 (Logghe M., unpublished) was exchanged by
15 the EcoRI-HindIII fragment, containing hIFNb flanked by two SfiI sites, from YCp50S-S (an E. coli / S. cerevisiae shuttle vector derived from the plasmid YCp50, which is deposited in the ATCC collection (number 37419; Thrash et al., 1985); an EcoRI-HindIII
20 fragment, containing the gene hIFNb, which is flanked by two SfiI sites, was inserted in YCp50, creating YCp50S-S), resulting into plasmid pMAL2PSiST-1. The MAL2 promoter from pMAL2PSiST-1 (by a NaeI-FspI digest) was further replaced by the GAL1 promoter from
25 pGAL1PNiST-1 (via a XhoI-SalI digest), creating the vector pGAL1PSiST-1.

Preparation of C. albicans genomic library

30 A C. albicans genomic DNA library with small DNA fragments was prepared for integrative disruption. Genomic DNA of C. albicans B2630 (ATCC No. 44858) was isolated following a modified protocol of Blin and Stafford (1976). To obtain enrichment for genomic DNA
35 fragments of the desired size, the genomic DNA was partially digested. Enrichment of small DNA fragments

- 18 -

was obtained with 70 units of AluI on 10 mg of genomic DNA for 20 min. T4 DNA polymerase (Boehringer) and dNTPs (Boehringer) were added to polish the DNA ends. After extraction with phenol-chloroform the digest was size-fractionated on an agarose gel. The genomic DNA fragments with a length of 0.5 to 1.25 kb were eluted from the gel by centrifugal filtration (Zhu et al., 1985). SfiI adaptors (5' GTTGGCCTTTT) were attached to the DNA ends (blunt) to facilitate cloning of the fragments into the vector. After ligation of these adaptors to the DNA fragments a second size-fractionation was performed on an agarose gel. The small genomic DNA fragments were cloned upstream of the GAL1 promoter in the vector pGAL1PSiST-1. Qiagen-purified pGAL1PSiST-1 plasmid DNA was digested with SfiI and the largest vector fragment eluted from the gel by centrifugal filtration (Zhu et al., 1985). The ligation mix was electroporated to MC1061 (...) E. coli cells.

C. albicans cDNA library

Total RNA was extracted from C. albicans strain B2630 grown on respectively minimal (SD) and rich (YPD) medium as described by Sambrook et al. (1989). mRNA was prepared from total RNA using the Invitrogen Fast Track procedure. First strand cDNA was synthesised with Superscript Reverse Transcriptase (BRL) and with an oligo dT-NotI Primer adapter. After second strand synthesis, cDNA was polished with Klenow enzyme and purified over a Sephacryl S-400 spin column. Phosphorylated SfiI adapters were then ligated to the cDNA, followed by digestion with the NotI restriction enzyme. The SfiI/NotI cDNA was purified and sized on a Biogel column A150M. cDNA was ligated in a NotI/SfiI opened pGAL1PNiST-1 vector.

- 19 -

Transformation of *C. albicans*

C. albicans CAI-4 (URA3::imm434/URA3::imm434) was kindly provided by Dr. William Fonzi, Georgetown University (Fonzi and Irwin, 1993). CAI-4 was transformed with above described cDNA library or genomic library using a modified spheroplast method (Logghe M., submitted). Cells were plated on minimal medium supplemented with glucose and sorbitol (SD (0.67% Yeast Nitrogen base w/o amino acids + 2% glucose), 1 M sorbitol) plates using 0.4 cm glass-pearls (Glaverbel, Belgium) and incubated for 2-3 days at 30°C.

Screening for mutants

Starter cultures were set up by inoculating each colony in 1 ml SD medium and incubating overnight at 30°C and 300 rpm. Cell densities were determined using a Coulter counter (Coulter Z1; Coulter electronics limited). 250.000 cells/ml were inoculated in SD medium for a total volume of 1ml and cultures were incubated for 24 hours at 30°C and 300 rpm. Cultures were washed in minimal medium without glucose (S) and the pellet resuspended in 650 ml S medium. 8 µl of this culture was used for inoculating 400 µl cultures in a Honeywell-100 plate (Bioscreen analyzer, Labsystems). Each transformant was grown for three days in S medium containing 50 mM LiAc; pH 6.0, with 2% glucose +/- 2% maltose or 2% galactose +/- 2% maltose respectively while shaking (high intensity) every 3 minutes for 20 seconds. Optical densities were measured every hour and growth curves were generated automatically (Bioscreen analyzer; Labsystems).

Construction of LAC4/ pGAL1PNiST-1

- 20 -

pGAL1PNiST-1 vector was cut with StuI in order to release the stuffer fragment and subsequently dephosphorylated (CIP, Boehringer). Plasmid pRS1004, obtained from J. Ernst (University of Duesseldorf, Germany), was cut with PvuII/XbaI in order to release the K. lactis β -galactosidase (EC 3.2.1.23; LAC4) reporter gene and Klenow-treated. The LAC4 PvuII/XbaI blunted reporter gene fragment from pRS1004 was ligated into StuI opened pGAL1PNiST-1 resulting in the integrative plasmid LAC4/ pGAL1PNiST-1

Measurement of GAL1 promoter activity

C. albicans strain CAI-4 was transformed with LAC4/pGAL1pNiST-1 using the modified spheroplast method (Logghe et al., submitted). Resulting transformants were grown in 5 ml of respectively non-induction (SD +/- maltose) and induction (S+ galactose +/- maltose) medium and further processed as described by Leuker et al. (1997).

Isolation of genomic or cDNA inserts

Potentially interesting transformants were grown in 1.5 ml SD overnight. Genomic DNA was isolated using the Nucleon MI Yeast kit (Amersham) and the concentration of genomic DNA was estimated by analyzing a sample on a 0.7% agarose gel in 0.5x TBE and comparison to a known standard molecular weight marker. 20 ng of genomic DNA was digested for three hours with an enzyme that cuts uniquely in the library vector (SacI for the genomic library; PstI for the cDNA library), treated with RNase A (Boehringer) and incubated for 20 minutes at 65°C to inactivate the enzyme. Samples were phenol/chloroform extracted twice and precipitated using NaOAc/ethanol. The resulting

- 21 -

pellet was resuspended in 500 μ l ligation mixture (1 x ligation buffer and T4 DNA ligase; both from Boehringer) and incubated overnight at 16°C. After denaturation (10 min 65°C), purification (phenol/chloroform extraction) and precipitation (NaOAc/ethanol) the pellet was resuspended in 10 μ l MilliQ (Millipore) water.

Inverse PCR was performed on 1 μ l of the precipitated ligation reaction using library vector specific primers (Figure 1) (3pGALSistPCR: 5' GAG-GGC-GTG-AAT-GTA-AGC-GTG 3' and 5pGALNistPCR: 5'GAG-TTA-TAC-CCT-GCA-GCT-CGA-C 3' for the genomic library; 3pGALNistPCR: 5' TGA-GCA-GCT-CGC-CGT-CGC-GC 3' and 5pGALNistPCR for the cDNA library; all primers from Eurogentec) for 30 cycles each consisting of (a) 1 min at 95 °C, (b) 1 min at 61 (or 57 °C for the cDNA library primers), and (c) 3 min at 72 °C. In the reaction mixture 2.5 units of Taq polymerase (Boehringer) with TaqStart antibody (Clontech) (1:1) were used, and the final concentrations were 0.2 μ M of each primer, 3 mM MgCl₂ (Perkin Elmer Cetus) and 200 μ M dNTPs (Perkin Elmer Cetus). All PCR reactions were performed in a Robocycler (Stratagene).

PCR analysis is also performed on genomic DNA isolated from the transformants using primers 3pGALSistPCR and 5pGALNistPCR for the genomic library transformants and using primers oligo23': 5' TGC-AGC-TCG-ACC-TCG-AGG 3' and oligo25: 5' GCG-TGA-ATG-TAA-GCG-TGA-C 3' (T_{hybr} = 53 °C) for the cDNA library transformants.

Resulting PCR products were purified using the PCR purification kit (Qiagen) and were quantified by comparison of band intensity with the intensity of DNA marker bands on a ethidium bromide stained agarose gel.

35

Sequence determination

- 22 -

The amount of PCR product (expressed in ng) put in the sequencing reaction is calculated as the length of the PCR product in basepairs divided by 10. DNA sequencing reactions were performed using the ABI Prism BigDye Terminator Cycle Sequencing Ready Reaction Kit according to the instructions of the manufacturer (PE Applied Biosystems, Foster City, CA) except for the following modifications. The total reaction volume was reduced to 15 μ l. Reaction volumes of individual reagents were changed accordingly. The 6.0 μ l Terminator Ready Reaction Mix was replaced by a mixture of 3.0 μ l Terminator Ready Reaction Mix + 3.0 μ l Half Term (GENPAK Limited, Brighton, UK). After cycle sequencing, reaction mixtures were purified over Sephadex G50 columns prepared on Multiscreen HV opaque Microtiter plates (Millipore, Molsheim, Fr) and were dried in a speedVac. Reaction products were resuspended in 3 μ l loading buffer. Following denaturation for 2 min at 95°C, 1 μ l of sample was applied on a 5% Long Ranger Gel (36 cm well-to-read) prepared from Singel Packs according to the supplier's instructions (FMC BioProducts, Rockland, ME). Samples were run for 7 hours 2X run on a ABI 377XL DNA sequencer. Data collection version 2.0 and Sequence analysis version 3.0 (for basecalling) software packages are from PE Applied Biosystems.

Sequence analysis

Nucleotide sequences were imported in the VectorNTI software package (InforMax Inc, North Bethesda, MD, USA), and the vector and insert regions of the sequences were identified. Sequence similarity searches against public and commercial sequence databases were performed with the BLAST software package (Altschul et al., 1990) version 1.4. Both the original nucleotide sequence and the six-frame conceptual translations of the insert region were used

- 23 -

as query sequences. The used public databases were the EMBL nucleotide sequence database (Stoesser et al., 1998), the SWISS-PROT protein sequence database and its supplement TrEMBL (Bairoch and Apweiler, 1998),
5 and the ALCES Candida albicans sequence database (Stanford University, University of Minnesota). The commercial sequence databases used were the LifeSeq® human and PathoSeq™ microbial genomic databases (Incyte Pharmaceuticals Inc., Palo Alto, CA, USA), and
10 the GENESEQ patent sequence database (Derwent, London, UK). Three major results were obtained on the basis of the sequence similarity searches: function, novelty, and specificity. A putative function was deduced on the basis of the similarity with sequences with a
15 known function, the novelty was based on the absence or presence of the sequences in public databases, and the specificity was based on the similarity with vertebrate homologues.

The 5' UTR region of the SAM2 gene was analysed using
20 the "Findpatterns" algorithm of the Genetics Computer Group (GCG) software package (University of Wisconsin, USA).

Northern blot analysis

25 Cells were grown to OD₆₀₀ ~ 1.0 and total RNA was prepared using the RNeasy midi kit (Qiagen) according to the manufacturer's instructions. RNA concentrations were determined spectrophotometrically by measuring optical densities at 260 nm in a UV-1601 UV-visible
30 spectrophotometer (Shimadzu) and 5 µg of each sample was resolved onto a 1% formaldehyde gel and run in 1 x formaldehyde gel running buffer (5prime-3prime) at 3.5 V/cm. RNA was stained for 20 minutes using SYBR Green II stain (Molecular probes) 1/10000 diluted in 1x
35 formaldehyde gel running buffer (5prime-3prime) and subsequently transferred to Hybond-N+ nylon membrane (Amersham) by overnight capillary blotting in 20 x

- 24 -

SSC. DIG-labeled probes were prepared using DIG-dUTP (Boehringer Mannheim) at a 1:3 or 1:6 dTTP:DIG-dUTP ratio, 10 pg of template plasmid DNA, 1x PCR buffer II (Perkin Elmer Cetus), 10 μ M of each primer (Eurogentec), 0.2 mM of dATP, dCTP and dGTP (Perkin Elmer Cetus), 2.5 mM MgCl₂ (Perkin Elmer Cetus), 5% DMSO and 1.25 units Taq polymerase (Boehringer). The membrane was prehybridized at 50°C (DNA probes) or at 68°C (RNA probes) in DIG Easy Hyb (Boehringer Mannheim) for minimum 1 hour. Hybridization was performed using 1 μ l PCR reaction product (= 1/50 of the total volume)/ml DIG Easy Hyb. The probes were denatured by heating the PCR reaction for 10 minutes at 96°C, then quick-chilling on ice. The probe was kept on ice for 5 minutes, centrifuged briefly and diluted in pre-warmed DIG Easy Hyb solution. The entire probe solution was filtered through a 0.45 μ m filter (Millex HV, Millipore) prior to use. Hybridizations were carried out overnight.

Post-hybridization, membranes were washed twice 15 minutes with 2x SSC/0.1% SDS at room temperature and twice 15 minutes with 0.1x SSC/0.1% SDS at 68°C. Detection was performed using the DIG Wash and Block Buffer Set as described by the manufacturer (Boehringer Mannheim Mannheim) and the blot was exposed to Kodak XAR-5 film for 1 hour at ambient temperature.

Real time quantitation of mRNA transcript PCR quantitations using specific primers and probes were performed according to the TaqMan procedure (Livak et al., 1995; Orlando et al., 1998) using the ABI Prism 7700 sequence detector (Applied Biosystems). Primers and probes for ACT1 (b-actin) and RNR1 genes were designed using the PrimerExpress software system (Perkin Elmer Cetus).

- 25 -

Cells were grown to OD₆₀₀ ~ 1.0 and total RNA was prepared using the RNeasy midi kit (Qiagen) according to the manufacturer's instructions. All RNA samples were DNaseI (Boehringer-Mannheim, RNase-free)-treated at 20 U/μg in 50 μl solution for 40 min at ambient temperature, phenol/chloroform-extracted and precipitated. Pellets were dissolved in 20 ml MilliQ water (Millipore) and RNA concentrations were determined spectrophotometrically. First-strand cDNA synthesis was performed in a final volume of 20 μl containing 1x Superscript RT buffer (Life Technologies), 10 mM DTT, 125 μM of each dNTP, 50 μM hexamer primers (Life Technologies) and 1 mg RNA. Mixtures were incubated for 10 min. at ambient temperature and 1 μl was removed and diluted 1:4 for the non-amplification control (NAC); 20 U Superscript reverse transcriptase (Life Technologies) was added and the reaction was incubated for 1 hour at 42 °C. The enzyme was inactivated for 10 min at 70°C. PCR reactions were set up in triplicate for all genes and contained 5 ml PCR buffer A, 4 mM MgCl₂, 200 μM each of dATP, dGTP, dCTP and 400 μM dUTP, 250 nM fluorogenic probe (for RNR1: 5' TGA-TCT-CAA-AAA-GTG-CTG-GAG-GAA-TCG-GT 3'), 0.5 U UNG, 1.25 U AmpliTaq Gold, 16.75 ml H₂O, 300 nM of appropriate FORWARD (for RNR1: 5' CGA-CAC-TTT-GAA-ATC-GTG-TGC-T 3') and REVERSE (for RNR1: 5' GCA-CCG-GTA-GAA-CGA-ATG-TTG 3') PCR primers, 1 ml of the RT reaction mixture. For the NAC, 1 μl of the 1:4 diluted RTase-negative sample was added while 1 μl of H₂O was added to each non-template control sample. The ABI PRISM 7700 was run for 50 cycles of 15 s at 95°C, 1 min at 60°C. These cycles were preceded by 5 min at 50°C (UNG activation) and 10 min at 95°C (UNG inactivation and DNA denaturation). Data were analyzed using the ABI PRISM 7700 software package. Data were normalized according to ACT1 C_T.

- 26 -

values.

Library screening

Using primers 5pGalNistPCR and 3pGalNistPCR, a 0.6 kb
5 region of the *C. albicans* SAM2 gene was PCR-amplified
from a SAM2/pGAL1pNiST-1 construct isolated from clone
36 and labeled with [³²P]dCTP using the Multiprime™
random-primed labeling system (Amersham). *C. albicans*
genomic DNA isolated from strain B2630 was partially
10 digested with Sau3AI, resolved on a 0.7% agarose gel
and the region of the gel with the fragment size of
interest (10-23kb) was cut out and DNA was eluted from
the gel with Sephaglass Band Prep kit (Pharmacia). A
C. albicans library in pYCP50 was prepared by ligating
15 these fragments into a BamHI cut and dephosphorylated
pYCP50 vector in a 1:2 molar ratio vector to insert.
The titer (#colonies/μg DNA) was determined by
transforming a fraction of the library to *E. coli*.
Five genome equivalents were plated out and filter-
20 lifts were prepared as described (Sambrook et al.,
1989). Duplicate nylon filters were pre-washed for 2
hours at 42°C in 50 mM Tris, 1M NaCl, 0.1% SDS, 1 mM
EDTA to reduce background hybridization. The filters
were subsequently hybridized at 42°C overnight in 5x
25 SSPE, 50% formamide, 5x Denhardt's solution, 0.1% SDS,
100 μg/ml denatured salmon sperm DNA and 10⁶ cpm/ml of
denatured probe. Filters were then washed in 2x SSC,
0.5 % SDS for 1 hour at room temperature and for 1
hour at 50°C. A few intense autoradiographic spots
30 were found and the corresponding colonies were
selected for plasmid preparation. Candidate clones
were digested with a panel of restriction enzymes,
resolved on a 0.7 % agarose gel, stained with
ethidiumbromide and transferred to nylon membrane by
35 vacuum-blotting. The blot was probed under the same
conditions as the genomic library. A 1.1 kb HpaI

- 27 -

fragment covering the entire hybridizing segment was subcloned into pCR-Blunt (Invitrogen)

5 **Screening for compounds modulating expression of polypeptides critical for growth and survival of *C. albicans***

 The method proposed is based on observations (Sandbaken et al., 1990; Hinnebusch and Liebman 1991; Ribogene PCT WO 95/11969, 1995) suggesting that
10 underexpression or overexpression of any component of a process (e.g. translation) could lead to altered sensitivity to an inhibitor of a relevant step in that process. Such an inhibitor should be more potent against a cell limited by a deficiency in the
15 macromolecule catalysing that step and/or less potent against a cell containing an excess of that macromolecule, as compared to the wild type (WT) cell.

 Mutant yeast strains, for example, have shown that some steps of translation are sensitive to the
20 stoichiometry of macromolecules involved. (Sandbaken et al.). Such strains are more sensitive to compounds which specifically perturb translation (by acting on a component that participates in translation) but are equally sensitive to compounds with other mechanisms
25 of action.

 This method thus not only provides a means to identify whether a test compound perturbs a certain process but also an indication of the site at which it exerts its effect. The component which is present in
30 altered form or amount in a cell whose growth is affected by a test compound is potentially the site of action of the test compound.

 The assay to be set up involves measurement of growth of an isogenic strain which has been modified
35 only in a certain specific allele, relative to a wild type (WT) *C. albicans* strain, in the presence of R-

- 28 -

compounds. Strains can be ones in which the expression of a specific essential protein is impaired upon induction of anti-sense or strains which carry disruptions in an essential gene. An in silico
5 approach to finding novel essential genes in *C. albicans* will be performed. A number of essential genes identified in this way will be disrupted (in one allele) and the resulting strains can be used for comparative growth screening.

10

Assay for High Throughput screening for drugs
35 μ l minimal medium (S medium + 2% galactose + 2% maltose) is transferred in a transparent flat-bottomed 96 well plate using an automated pipetting
15 system (Multidrop, Labsystems). A 96-channel pipettor (Hydra, Robbins Scientific) transfers 2.5 μ l of R-compound at 10^{-3} M in DMSO from a stock plate into the assay plate.

20 The selected *C. albicans* strains (mutant and parent (CAI-4) strain) are stored as glycerol stocks (15%) at -70°C . The strains are streaked out on selective plates (SD medium) and incubated for two days at 30°C . For the parent strain, CAI-4, the medium
25 is always supplemented with 20 $\mu\text{g/ml}$ uridine. A single colony is scooped up and resuspended in 1 ml minimal medium (S medium + 2% galactose + 2% maltose). Cells are incubated at 30°C for 8 hours while shaking at 250 rpm. A 10 ml culture is inoculated at 250.000
30 cells/ml. Cultures are incubated at 30°C for 24 hours while shaking at 250 rpm. Cells are counted in Coulter counter and the final culture (S medium + 2% galactose + 2% maltose) is inoculated at 20.000 to 50.000 cells/ml. Cultures are grown at 30°C while shaking at
35 250 rpm until a final PD of 0.24 (+/- 0.04) 6nM is reached.

200 μ l of this yeast suspension is added to all

- 29 -

wells of MW96 plates containing R-compounds in a 450 μ l total volume. MW96 plates are incubated (static) at 30°C for 48 hours.

Optical densities are measured after 48 hours.

5 Test growth is expressed as a percentage of positive control growth for both mutant (x) and wild type (Y) strains. The ratio (x/y) of these derived variables is calculated.

10

RESULTS

A *C. albicans* integrative vector, pGAL1PSiST-1, was constructed to allow non-directional cloning of *C. albicans* genomic DNA fragments (Figure 2). The vector contains an inducible GAL1 promoter, a SfiI-cloned stuffer fragment, a *C. albicans* URA3 selection marker and elements to allow autonomous replication and selection in *E. coli*. A *C. albicans* genomic DNA library was prepared by ligating small genomic DNA fragments (400 to 1000 bp) which were linked to SfiI adaptors into the SfiI opened vector pGAL1PSiST-1 vector. Genomic DNA fragments (450 ng) were ligated into the pGAL1PSiST-1 vector (20 ng). After electroporation into *E. coli* approximately 400,000 clones were obtained. Plasmid DNA was prepared of ... clones; 91% contained an insert with an average length of 600 bp. The size of the library corresponds to over 5 times the diploid genome with genomic DNA inserts oriented in sense or antisense direction in the vector.

30 A similar *C. albicans* integrative vector, pGAL1PNiST-1, was constructed to allow SfiI/Not I directional cloning of *C. albicans* cDNA fragments (Figure 2). The SfiI/NotI cDNA was purified and sized on a Biogel column A150M. The first fraction contained approximately 38,720 clones upon transformation to *E. coli* with an average insert size of 1500 bp. cDNA from this fraction was ligated into a NotI/SfiI opened pGAL1PNiST-1 vector.

- 30 -

C. albicans strain CAI-4 was transformed with the
aforementioned genomic and cDNA libraries. Upon
homologous recombination between the insert (partial or
complete gene) in a library clone and the corresponding
5 gene in the Candida genome, this gene is (partially if
the gene is not full-length) duplicated (Figure 1). The
first copy of the gene is flanked upstream by its native
promoter and downstream by the GAL1 promoter. The
10 direction of transcription from the native promoter is
opposite to that of the GAL1 promoter. Induction of the
GAL1 promoter might thus lead to altered expression of
the gene at the integration site. Moreover, if the cDNA
does not contain the entire 5' coding region, the first
15 copy of the gene may not give rise to any more to a
functional protein. The second copy of this gene has
lost its promoter and will therefore not be transcribed
(Figure 1).

Upon integration at the site of the GAL1 promoter,
the promoter is duplicated yielding an integrated gene
20 fragment under control of the GAL1 promoter (Figure 1).

Growth curves were measured in the presence of
lithium acetate. Figure 3 shows growth curves of the
wild type CAI-4 strain and transformants -resulting from
cDNA library transformation- showing either an overall
25 impaired growth (clone 38; Figure 3C) or galactose-
induced (clone 36; Figure 3B) reduction in growth. This
analysis was performed in S-glucose medium as a non-
induction medium and S-galactose medium as an induction
medium. The results shown in Figure 3A show that also
30 the wild type strain shows reduced growth in antisense
induction medium. This is because galactose is used
rather inefficiently as a carbon source by C. albicans.
In order to solve this problem and facilitate the
selection procedure an extra carbon source, maltose, was
35 added to both inducing and non-inducing medium. Again
growth patterns varied significantly from transformant
to transformant but growth of the parental strain CAI-4

- 31 -

was nearly identical in both media (Figure 3D). Strains impaired in growth upon promoter activation showed a clear shift in the growth curve in medium supplemented with both galactose and maltose (clone 415; Figure 3E).
5 Overall impaired growth was, as expected, not strongly influenced by the addition of maltose (clone 360; Figure 3F).

To verify that maltose as an extra carbon source did not affect the strength and inducibility of the GAL1 promoter, promoter activity was measured using
10 Kluyveromyces lactis LAC4 reporter gene expression. CAI-4 was transformed with LAC4/pGAL1pNiST-1. Four individual transformants (named Q, R, S, T) were grown in glucose, galactose, glucose+maltose and
15 galactose+maltose media and β -galactosidase activity was measured (Figure 4). It is clear that the presence of maltose does not significantly influence the induction ratio of the GAL1 promoter.

From a total of over 2000 transformants screened,
20 198 (~10%) showed an impaired growth phenotype and were selected for further analysis. Forty-three % of these slow growers showed a growth pattern corresponding with a putative promoter interference or antisense effect, 57% showed overall impaired growth. PCR analysis with
25 5pGALNiSTPCR and 3pGALNiSTPCR primers on genomic DNA from the transformants can reveal integration outside the gene showing sequence identity with the insert DNA, eg. at the GAL1 promoter region (Figure 1). Of all transformants screened by PCR using these primers,
30 ~ 11% showed integration at a non-insert location.

When the insert of an antisense library clone recombines with the homologous gene in the *C. albicans* genome, no PCR product can be obtained upon
35 amplification with 5pGALNiSTPCR and 3pGALNiSTPCR primers on genomic DNA (Figure 1). To release the plasmid from the genome and determine the integration site, genomic DNA was isolated from the transformants, cut (with SacI

- 32 -

for the genomic library transformants and with PstI for the cDNA library transformants), religated and the resulting ligation reaction was precipitated and used as a template for inverse PCR. This procedure reveals homologous integration at the insert site as well as the number of integrations (assuming PCR products are of different lengths) within the *Candida* genome. This analysis was performed on all selected transformants, ~32 % of which showed multiple integrations. The frequency of multiple integrations was very variable and depended on the batch of transformants analyzed. The resulting PCR products from both analyses were subsequently sequenced and the sequences compared with both public and proprietary sequence databases. In total 86 different genes could be identified, 45 of which were of unknown function.

For the CAI-4 transformants obtained with a genomic (non-directionally cloned) library, 26% of the selected clones (n=~150) contained the *C. albicans* autonomous replicating sequence, ARS2, and 15% of the clones contained a ribosomal RNA fragment.

For the CAI-4 transformants obtained with a cDNA library (n=~1850) a whole series of different gene fragments was found. As expected, also a number of genes involved in carbon source metabolism and nutrient uptake were identified.

Two examples of identified genes will be discussed, although as seen in Figures 16 to 70 similar results were obtained for all of the sequences according to the invention. Clone 36 shows a galactose-induced impairment in growth, suggestive of a promoter interference or antisense effect (Figure 3B). In this clone recombination had occurred at the insert site as shown by amplification of a ~600bp gene fragment by inverse PCR. The sequence of the isolated gene fragment was 74 % identical to a *S. cerevisiae* S-adenosyl methionine synthetase 2 (SAM2) gene. Effects on SAM2 mRNA were

- 33 -

assessed by Northern blots on total RNA extracted from a non-transformed control strain and from clone 36 grown either in antisense-inducing or non-inducing media. The Northern blot was hybridised with an in vitro synthesized SAM2 RNA sense probe to detect antisense transcripts (Figure 5). An identical Northern blot was hybridised with an in vitro synthesized SAM2 antisense probe to detect SAM2 mRNA (Figure 5). Both blots were subsequently hybridized with a TEF3 DNA probe to allow normalization. As the sequence of the *C. albicans* SAM2 gene was not available at the time, a *C. albicans* genomic library in pYCp50 was prepared and *E. coli* transformants were screened for the full-length gene using the 600 bp SAM2 PCR fragment as a probe. A strongly hybridizing clone was identified and designated clone 36.13.1. This clone contained the complete ORF (1155 bp) of the SAM2 gene including 5' and 3' flanking regions. In the very A/T-rich 5' flanking region a putative TATA box could be identified at -27 bp. The 3' flanking region contains multiple T-rich (>10 bp) regions, elements described in yeast as necessary for transcript release (Reeder and Lang, 1997). The complete SAM2 mRNA transcript thus has a predicted length of 1.2 kb.

Clone 38 showed impaired growth in both non-inducing and inducing media (Figure 3); this is expected when integration of the library plasmid itself leads to gene suppression. Clone 38 contained a 340 bp fragment of the ribonucleotide reductase 1 (RNR1) gene. RNR1 mRNA levels were analysed by Northern blot and quantitative PCR in a non-transformed control strain and clone 38 grown in S+glucose medium. The Northern blot was hybridised successively with an actin and an RNR1 doublestranded DNA probe (Figure 6). Although the β -actin transcript level in the control strain is lower compared to clone 38, the relative amount of RNR1 transcript is higher, indicating a reduced level of RNR1

- 34 -

transcript in clone 38. This result was confirmed by Taqman quantitative PCR on both control strain and clone 38 using a RNR1 fluorogenic probe. Resulting Ct values were calculated and normalised for β -actin (Figure 6).
5 Again RNR1 transcript levels in clone 38 were found reduced compared to the control strain.

To verify that the growth-effect was due to the interference with the identified gene and to support the specificity of the antisense effect, single allele knock-outs were made in 6 identified genes using the URA-blaster method (Fonzi and Irwin, 1993). Disruption of one allele of a gene should in theory lead to ~ 50 % reduction in gene transcript. In practice however we have observed reductions varying between 10 and 100 %
10 of normal level. This can probably be explained by the fact that not always both copies of a gene are functional. That only a single integration at the correct site had occurred for each of the disruption cassettes was verified by PCR and Southern blot
15 analysis. Growth curves were measured; three disruptants showed impaired growth, suggesting that a gene required for growth or survival was targeted. Experiments to take over control of the second allele of each gene -by promoter replacement- are ongoing.

25 The present application describes new methods to diminish endogenous gene expression in the medically important yeast *C. albicans*. Our approach proved very useful for the identification of genes required for growth or survival. Technical hurdles consisted of the
30 lack of an efficient transformation method for *C. albicans* (Logghe M., submitted) and the need to measure growth reproducibly on a large number of transformants in parallel. The latter was achieved with a Bioscreen Analyzer (Labsystems) which can simultaneously measure
35 growth in 200 cultures and subsequently generate growth curves automatically. Although in principle this kind of screening could be done on plates we could not

- 35 -

achieve satisfactory reproducibility using plate screening.

5 In our genomic screen, integration of the library plasmid can happen either at the endogenous GAL1 promoter locus or, more frequently, at the locus
10 corresponding to the plasmid insert. The latter results in a gene duplication with the first copy of the gene flanked by two convergently oriented promoters. The use of such a "collision construct" has previously been described in screening for inhibitors of transcriptional
15 activation in mammalian cells (patent WO 97/10360; Giese K.). If RNA polymerase II complexes start from both the upstream and downstream, oppositely oriented, promoter regions, they may collide thereby preventing the formation of a full-length mRNA transcript. The second
20 copy of the gene has no more a promoter and is probably 5' crippled as the original inserts cloned into the library have an average length of ~1.5 kb while ORFs in *C. albicans* have an average length of ... and we ourselves identified ORFs of (unknown) genes larger than 7 kb.

Upon integration of a plasmid into the *C. albicans* genome, reduced function of the protein encoded by the disrupted gene can be due to several mechanisms: 1) The
25 first copy of the duplicated gene can be prevented from forming functional sense transcript by promoter collision or the sense transcript may be inhibited by true antisense. Indeed, although a 1.2 kb SAM2 antisense transcript could be detected in clone 36 we cannot exclude the growth defect being due to promoter
30 interference. If an antisense transcript is formed from an intact SAM2 gene, we expect a transcript of at least 1055 bp; no transcription terminator was engineered upstream of this gene so transcription will proceed until an appropriate transcription termination
35 recognition site is reached. The promoter region of the SAM2 gene is particularly A/T rich and contains a reversed yeast transcription terminator site at - 118

- 36 -

(with translation starting at +1). In yeast, transcription terminator sites are ill-defined but for a T-rich stretch with non-T residues situated appropriately to prevent slippage (Jeong et al., 1996; Reeder and Lang, 1997). If termination of transcription occurs at this theoretically predicted site, a 1.17 kb transcript would be expected, as was found. 2) If mutations were present in the original library clone, the protein encoded by the gene after homologous recombination could be non-functional. 3) Possible cis down-regulatory effects on adjacent genes could be induced upon integration of large DNA fragments at certain locations within the genome. 4) Finally, gene disruption could occur by recombination with cDNA that is not full-length at the 5' end.

If -on the contrary- integration happens at the endogenous GAL1 promoter site, the GAL1 promoter is duplicated and antisense can be induced from this promoter. Promoter collision is not possible as the endogenous promoter of the gene is lacking at the integration site. Integration at a non-homologous site within the genome is rare. Transformation efficiencies of 0.7-3 transformants/ μ g have been reported upon transformation of CAI-4 with non-homologous plasmid DNA (Thompson et al., 1998). Also, integration at the URA3 locus is very unlikely as the complete URA3 gene has been removed from the CAI-4 genome.

Irrespective of the mechanism responsible for gene suppression, we could identify genes required for growth or survival by screening for transformants showing either galactose-induced or complete growth block. Furthermore, for such genome-wide screening no prior sequence information is needed and it allows discovery of possibly new critical functions. However, some genes may only be critical under conditions different from growth in minimal medium (as used in our screening) e.g. environments with high oxygen tension, high osmolarity

- 37 -

or high pH. However, it would be possible to screen for a growth phenotype under these conditions using our screening method. Alternatively, some genes may play critical roles only under unusual growth states or may specifically be required for adaptation to conditions encountered during infection of a host.

More than half of the ORFs we have identified as being critical for growth have a completely unknown function. Even though required for growth in *C. albicans*, for some genes no homologues could be found in existing databases, suggesting that they are species-specific genes. Indeed, recent genome sequencing efforts (e.g. *Mycoplasma genitalium* (Fraser et al., 1995), *Haemophilus influenzae* (Fleischmann et al., 1995)) have shown that approximately 20 % of the predicted ORFs in a microbial genome can be species-specific.

One disadvantage of the technique is that multiple library plasmids can integrate in the genome of a single *C. albicans* cell. When this occurs, identification of the target responsible for the growth defect becomes more difficult. Also, as shown in *Schizosaccharomyces pombe* (Atkins et al., 1995), RNA-mediated suppression may not be effective for certain genes, which we would miss when relying only on this technique.

Rather unexpectedly, transformation with the genomic library and subsequent screening for transformants showing reduced growth frequently yielded ARS2- and rRNA-containing clones (in 26 and 15% respectively of the transformants showing reduced growth). Previously, a study of aging yeast mother cells had shown that accumulation of extrachromosomal rDNA circles (ERCs) occurs in old cells and that these ERCs actually cause aging (Sinclair et al., 1997; Johnson et al., 1999). rDNA is present at 100-200 tandem copies on chromosome XII of *S. cerevisiae* and was found to accumulate to about 1000 copies in senescent cells. One other gene we identified is a homologue of the

- 38 -

essential *S. cerevisiae* gene TRA1, a protein kinase showing highest identity to the human TRRAP gene (McMahon et al., 1998) which is an ataxia telangiectasia mutated (ATM)-related gene. Loss of ATM is a genetic defect identified in ataxia telangiectasia (Johnson et al., 1999), a disease in humans where life span is typically reduced to 40-50 years. We might thus have picked up a number of growth-inhibitory effects due to induction of aging.

The strategy presented should be applicable to all organisms for which existing techniques for "en masse" gene disruption are not easily applicable because of their diploid nature and lack of sexual cycle and might prove especially useful for other diploid imperfect yeasts.

Although the genomic strategy that we described cannot substitute for a comprehensive investigation of individual genes and pathways, it can provide a good starting point for such investigation.

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1016.
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- 45 -

TABLE 1

	<u>Seq ID No.</u>	<u>Clone</u>	<u>Function</u>
5	1	214c_cpL1	-
	2	113g2	-
	3	222g8	-
	4	222g8(prt)	-
10	5	222g9	-
	6	222g9_CDS_1	-
	7	222g9_CDS_2	-
	8	222g9_CDS_3	-
	9	222g9_CDS_4	-
15	10	24gG	-
	11	28gK	-
	12	328c1	-
	13	328c1(prt)	-
	14	33gK	-
20	15	33gK(prt)	-
	16	3gG	-
	17	58gA	-
	18	21g2	-
	19	21g2(prt)	5' UTR TRA1
25	20	223c_cp	CFL
	21	357cL	
	22	357cL(prt)	RPL27
	23	110c_af	
	24	110c_af(prt)	SADH
30	25	CDC48	
	26	CDC48(prt)	CDC48
	27	99g3	
	28	99g3(prt)	CIT
	29	ESP1	
35	30	ESP1(prt)	ESP1
	31	190g3	
	32	190g3(prt)	FAL1
	33	249c_af	
	34	249c_af(prt)	MAA
40	35	485cL	
	36	485cL(prt)	RPL16
	37	328c3	
	38	328c3(prt)	RPS21
	39	83c3	
45	40	83c3(prt)	SHA3
	41	233c_cp2	
	42	233c_cp2	TPI1
	43	214c_cpL1	HXT6_2
	44	128g4	15S rRNA
50	45	135g	tRNA_Ser

- 46 -

	<u>Seq ID No.</u>	<u>Clone</u>	<u>Function</u>
5	46	22g3	
	47	22g3_CDS1	
	48	22g3_CDS2	-
	49	38g1	-
	50	117c_af	-
10	51	117c_af(prt)	-
	52	17g1	-
	53	17g1_CDS1	-
	54	17g1_CDS2	-
	55	480c	-
15	56	480c(prt)	-
	57	55g3	-
	58	55g3(prt)	-
	59	61gB	
	60	61gB(prt)	PSP2
20	61	62gB	
	62	62gB(prt)	-
	63	80g3	
	64	80g3(prt)	-
	65	29g2_part1	
25	66	29g2_part1(prt)	EF4
	67	29g2_part2_3	
	68	29g2_part2(prt)	EF4
	69	29g2_part3(prt)	EF4
	70	226c_af2	
30	71	226c_af2(prt)	ADE12
	72	409c5	
	73	409c5(prt)	HOL1
	74	40c_af	
	75	40c_af(prt)	FBP
35	76	55g1	
	77	55g1(prt)	MEG1
	78	67g1	
	79	67g1(prt)	RVS167
	80	232c_cp	
40	81	360c6	
	82	360c6(prt)	HXT6_1
	83	98c_cp	
	84	98c_cp(prt)	KGD2
	85	17c_cp	
45	86	17c_cp(prt)	NDE1
	87	60gK	
	88	60gK(prt)	RAD18
	89	226c_af1	
	90	226c_af1(prt)	-
50	91	328c2	
	92	328c2(prt)	-
	93	498c_cp	

- 47 -

	<u>Seq ID No.</u>	<u>Clone</u>	<u>Function</u>
5	94	498c_cp(prt)	-
	95	64gB	
	96	64gB(prt)	-
	97	8c_cp	
	98	8c_cp(prt)	-
10	99	15c1	
	100	15c1(prt)	-
	101	233c_cp1	
	102	233c_cp1_CDS1	
	103	233c_cp1_CDS2	-
15	104	35gK	
	105	35gK(prt)	-
	106	36g2	
	107	36g2(prt)	-
	108	65g	
20	109	65g(prt)	-
	110	85g3	
	111	85g3(prt)	
	112	232c_cp(prt)	SAP
	113	409c10	
25	114	409c10(prt)	-

KNOCK-OUT DATA SHEET

A. FAL1 single allele knock-out

Correct and single integration of FAL1 disruption cassette was confirmed by both PCR and Southern blot analysis (see support data on CD-ROM)

1. Analysis on RNA level

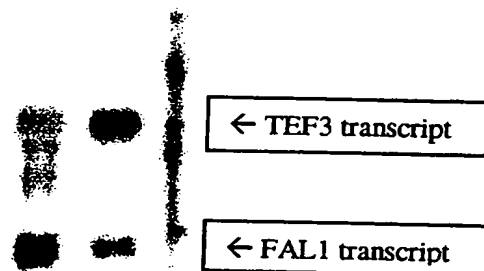
Northern blot analysis:

Lane 1: RNA MWM I (Boehringer Mannheim)

Lane 2: WT + gal + mal + LiAc

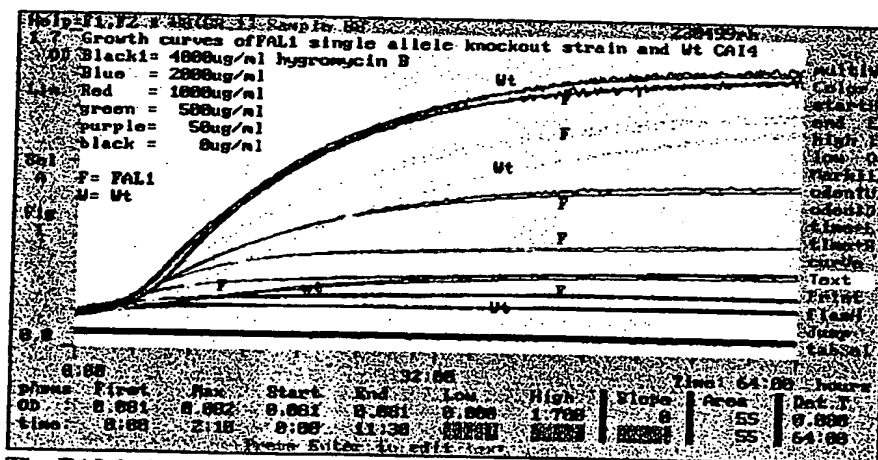
Lane 3: FAL1 + gal + mal + LiAc

Lane 4: RNA MWM I DIG labeled (Boehringer Mannheim)



Lower FAL1 transcript levels are observed in the FAL1 single allele knock-out strain compared to the wild type strain.

2. Growth analysis



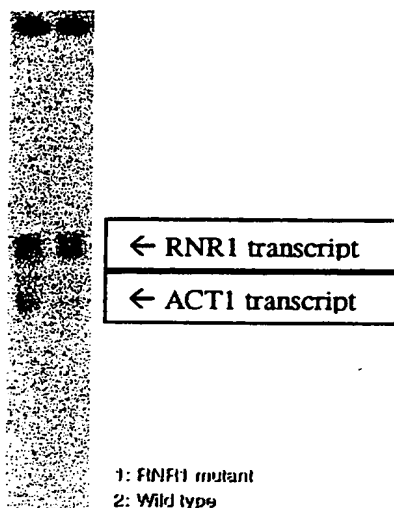
The FAL1 single allele knock-out grows equal to the wild type, however it is significantly more resistant to Hygromycin B.

B. RNR1 single allele knock-out

Correct and single integration of RNR1 disruption cassette was confirmed by both PCR and Southern blot analysis (see support data on CD-ROM)

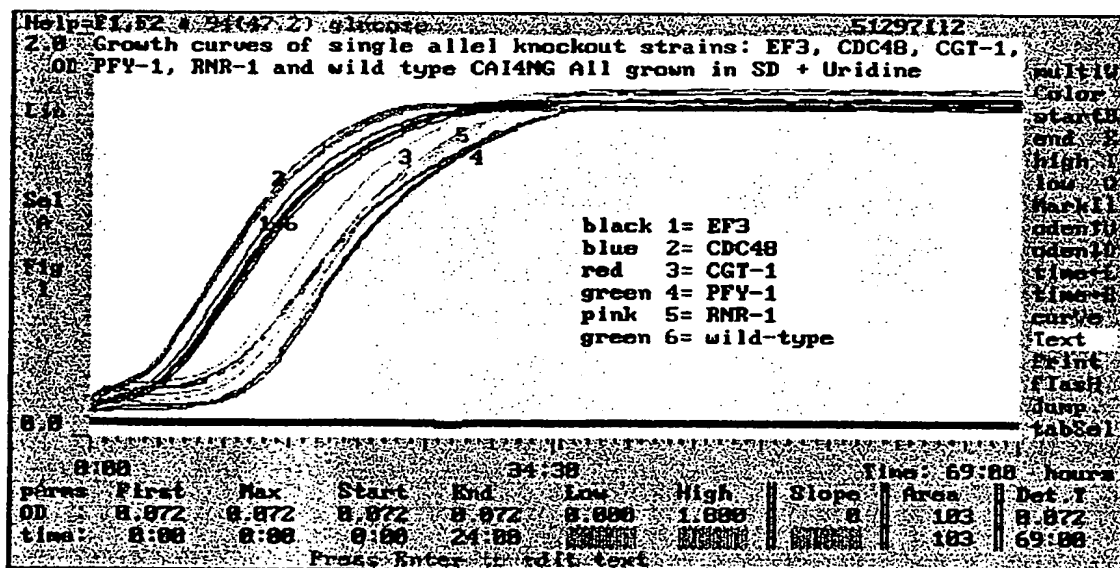
1. Analysis on RNA level

Northern blot analysis:



Lower RNR1 transcript levels are observed in the RNR1 single allele knock-out strain compared to the wild type strain. This result was confirmed by quantitative PCR (QT-PCR).

2. Growth analysis



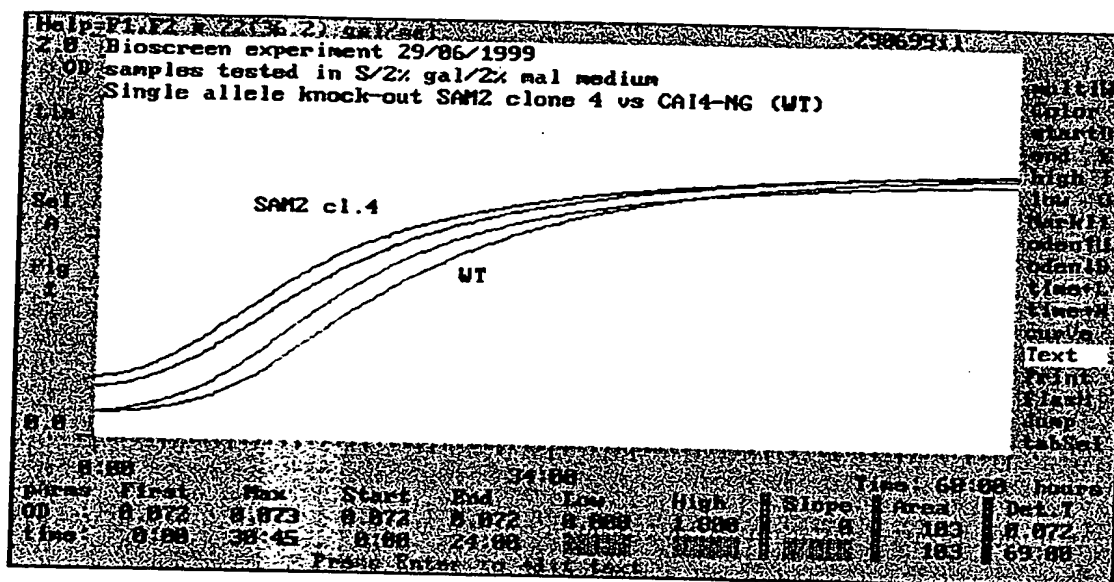
C. SAM2 single allele knock-out

Correct and single integration of SAM2 disruption cassette was confirmed by both PCR and Southern blot analysis (see support data on CD-ROM)

1. Analysis on RNA level

Northern blot analysis:

2. Growth analysis



Inoculum for SAM2 was somewhat higher; at equal inocula growth of SAM2 single allele knock-out is slightly slower.

E. MEG1 single allele knock-out

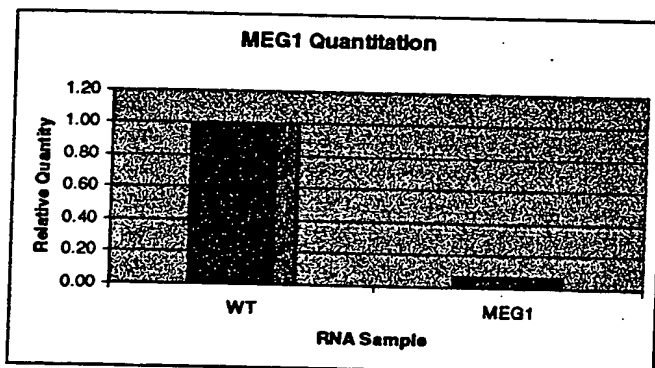
Correct and single integration of MEG1 disruption cassette was confirmed by both PCR and Southern blot analysis (see support data on CD-ROM)

1. Analysis on RNA level

QT-PCR analysis:

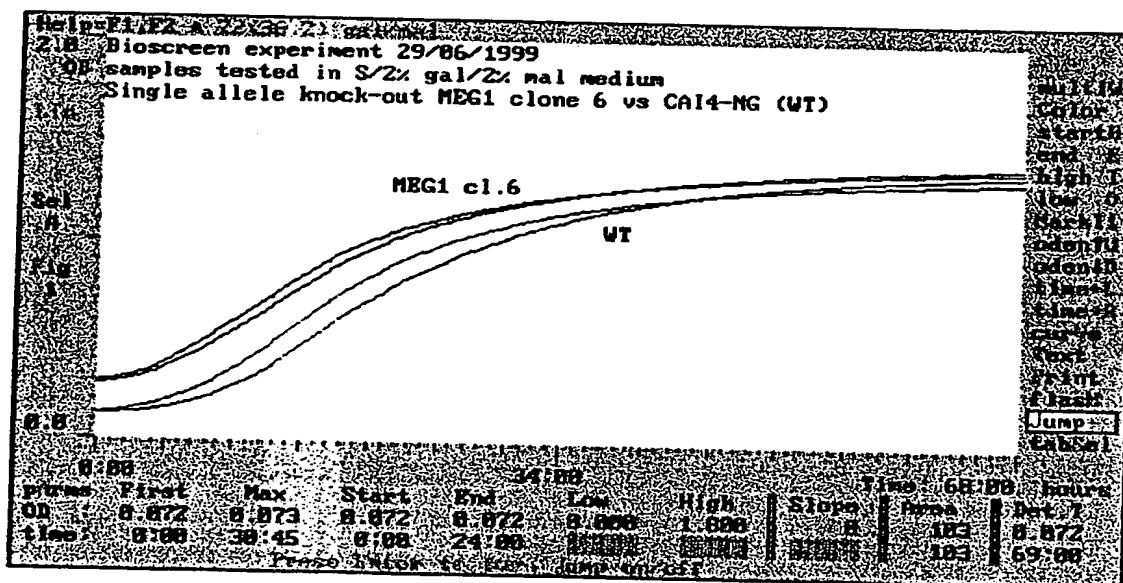
Relative quantitation for MEG1 vs. Act

	Avrg. MEG1	Avrg. ACT	dCt	ddCt	2-ddct
WT	35.79	33.49	2.29	0.00	1.00
MEG1	38.62	32.57	6.05	3.76	0.07



MEG1 expression was decreased more than 14 fold in the MEG1 single allele knock-out compared to the Wt.

2. Growth analysis



Inoculum for SAM2 was somewhat higher; at equal inocula growth of SAM2 single allele knock-out is slightly slower.

F. MAA single allele knock-out

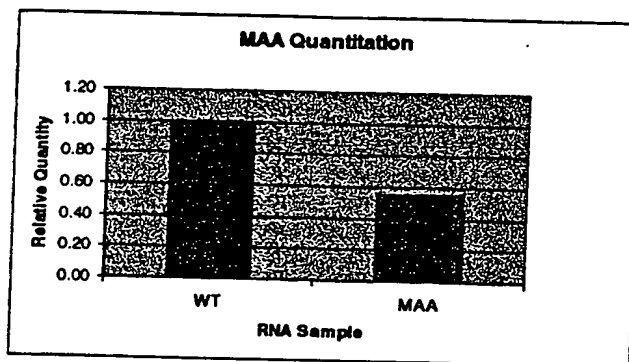
Correct and single integration of MAA disruption cassette was confirmed by both PCR and Southern blot analysis (see support data on CD-ROM)

1. Analysis on RNA level

QT-PCR analysis:

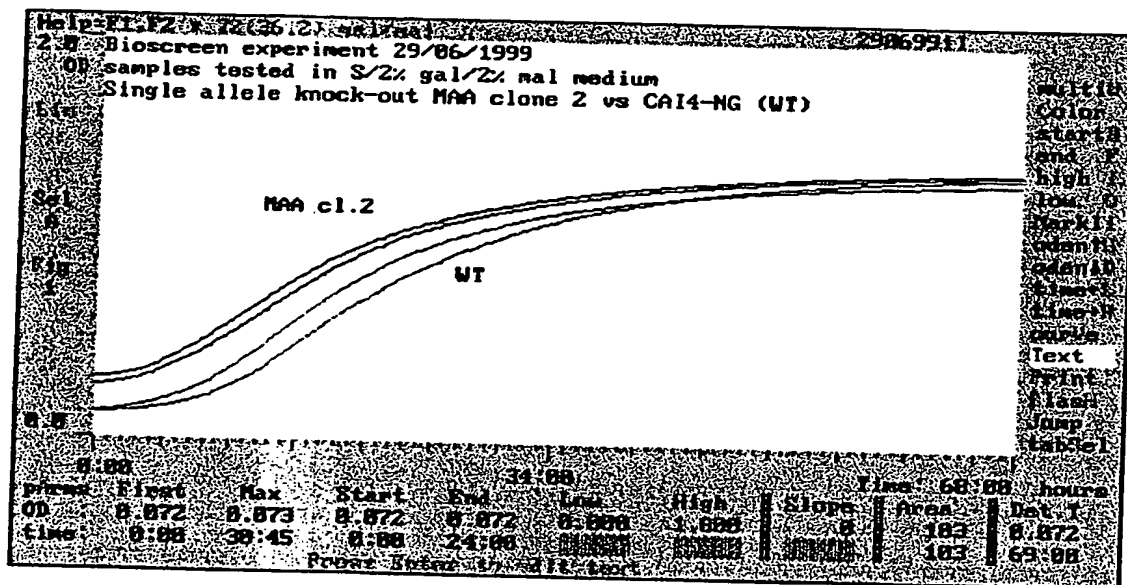
Relative quantitation for MAA vs. Act

	Avrg. MAA	Avrg. ACT	dCt	ddCt	2-ddct
WT	34.85	33.49	1.36	0.00	1.00
MAA	32.86	30.64	2.22	0.86	0.55



MAA expression was decreased two fold in the MAA knock-out compared to the Wt.

2. Growth analysis



Inoculum for MAA was somewhat higher; at equal inocula growth of MAA single allele knock-out is slightly slower.

G. RPL27 single allele knock-out

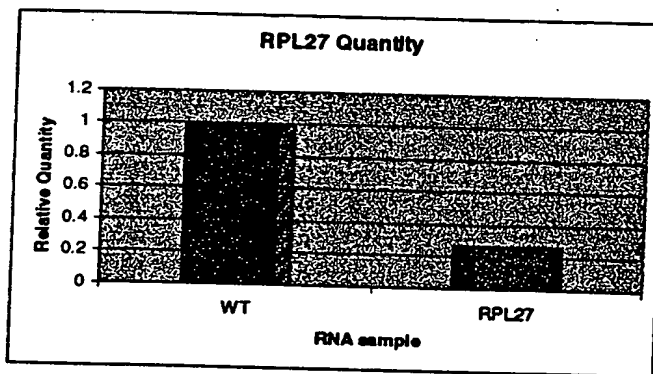
Correct and single integration of RPL27 disruption cassette was confirmed by both PCR and Southern blot analysis (see support data on CD-ROM)

1. Analysis on RNA level

QT-PCR analysis:

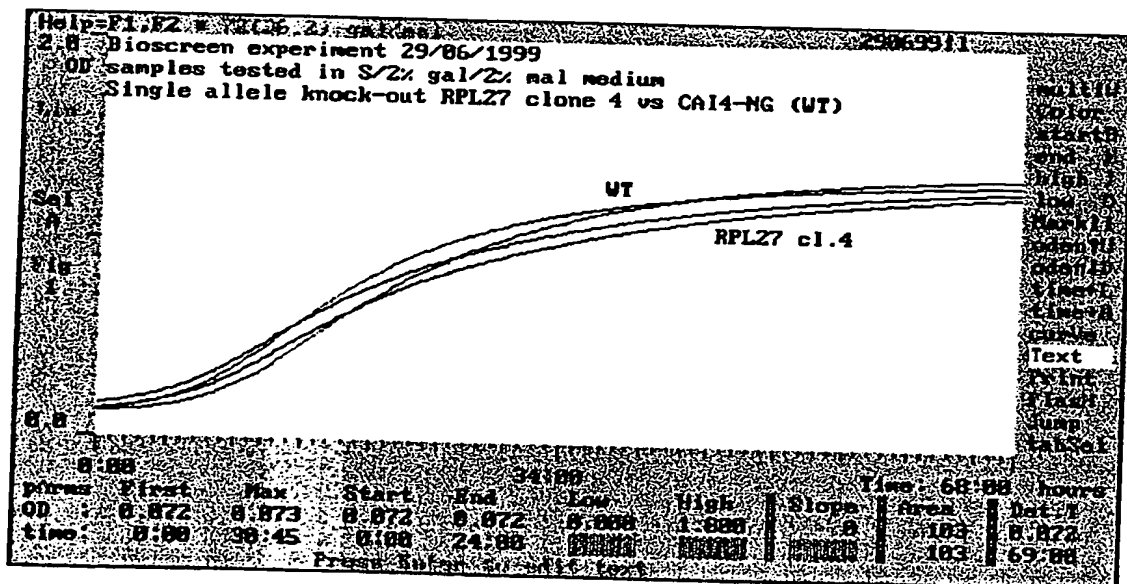
Relative quantitation for RPL27 vs. Act

	Avrg. RPL27	Avrg. ACT	dCt	ddCt	2-ddct
WT	33.01	33.49	-0.48	0.00	1
RPL27	34.37	32.98	1.39	1.87	0.27



RPL27 expression was decreased more than three fold in the RPL27 knock-out compared to the Wt.

2. Growth analysis



The RPL27 single allele knock-out grows equally to the wild type strain.

- 55 -

Claims

1. A nucleic acid molecule encoding a polypeptide which is critical for survival and growth of the yeast *Candida albicans* and which nucleic acid molecule comprises any of the sequences of nucleotides in Sequence ID Numbers 1, 2, 3, 5, 10, 11, 12, 14, 16, 17, 18, 20, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 44, 45, 46, 49, 50, 52, 55, 57, 59, 61, 63, 65, 67, 70, 72, 74, 76, 78, 80, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 104, 106, 108, 110 and 113 or the sequences of nucleotides identified in Figures 9 to 13.
2. A nucleic acid molecule encoding a polypeptide which is critical for survival and growth of the yeast *Candida albicans* and which nucleic acid molecule comprises any of the sequences of nucleotides in Sequence ID Numbers 1, 2, 3, 5, 10, 11, 12, 14, 16, 17, 18, 46, 49, 50, 52, 55, 57, 59, 61, 63, 65, 87, 89, 91, 93, 95, 97, 99, 101, 104, 106, 108, and 110, or fragments or derivatives of said nucleic acid molecules.
3. A nucleic acid molecule encoding a polypeptide which is critical for survival and growth of the yeast *Candida albicans* and which nucleic acid molecule comprises any of the sequences of nucleotides in Sequence ID Numbers 20, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 45, 65, 70, 72, 74, 76, 78, 80, 81, 83, 85, 113, and fragments or derivatives of said nucleic acid molecules.
4. A nucleic acid molecule encoding a polypeptide which is critical for survival and growth of the yeast *Candida albicans* and which nucleic acid molecule comprises any of the sequences of nucleotides of sequence ID Nos 1 and 91.

- 56 -

5. A nucleic acid molecule encoding a polypeptide which is critical for survival and growth of the yeast *Candida albicans* and which polypeptide has an amino acid sequence according to the sequence of any of Sequence ID Numbers 4, 6 to 9, 13, 15, 19, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 43, 47, 48, 51, 53, 54, 56, 58, 60, 62, 64, 66, 68, 69, 71, 73, 75, 77, 79, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 103, 105, 107, 109, 111, 112, and 114 or the sequences identified in Figures 14 and 15.

6. A nucleic acid molecule according to any one of claims 1 to 5 which is mRNA.

7. A nucleic acid molecule according to any of claims 1 to 5 which is DNA.

8. A nucleic acid molecule according to claim 7 which is cDNA.

9. A nucleic acid molecule capable of hybridising to the molecules according to any of claims 1 to 5 under high stringency conditions.

10. A nucleic acid molecule according to claim 9 which is an antisense molecule.

11. A polypeptide encoded by the nucleic acid molecule according to any of claims 1 to 8.

12. A polypeptide which is critical for survival and growth of the yeast *Candida albicans* having the amino acid sequences of any of Sequence ID Numbers 4, 6 to 9, 13, 15, 19, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 43, 47, 48, 51, 53, 54, 56, 58, 60, 62, 64, 66, 68, 69, 71, 73, 75, 77, 79, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 103, 105, 107, 109, 111, 112, and 114.

- 57 -

13. A polypeptide according to claim 12 having an amino acid sequence of any of Sequence ID Numbers 4, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 66, 68, 69, 71, 73, 75, 77, 79, 82, 84, 86 and 114.

5

14. A polypeptide according to claim 12 having an amino acid sequence of any of Sequence ID Nos 43 or 92.

15. An expression vector comprising a nucleic acid molecule according to claim 7 or 8.

10

16. An expression vector according to claim 15 which comprises an inducible promoter.

17. An expression vector according to claim 15 or 16 which comprises a sequence encoding a reporter molecule.

15

18. A nucleic acid molecule according to any of claims 1 to 10 for use as a medicament.

20

19. Use of a nucleic acid molecule according to any of claims 1 to 10 in the preparation of a medicament for treating *Candida albicans* associated diseases.

25

20. A polypeptide according to any of claims 11 to 14 for use as a medicament.

21. Use of a polypeptide according to any of claims 11 to 14 in the preparation of a medicament for treating *Candida albicans* associated infections.

30

22. A pharmaceutical composition comprising a nucleic acid molecule according to any of claims 1 to 10 or a polypeptide according to any of claims 11 to 14 together with a pharmaceutically acceptable carrier diluent or excipient therefor.

35

- 58 -

23. A *Candida albicans* cell comprising an induced mutation in the DNA sequence encoding a polypeptide according to any of claims 11 to 14.

5 24. A method of identifying compounds which selectively modulate expression of polypeptides which are crucial for growth and survival of *Candida albicans*, which method comprises:

10 (a) contacting a compound to be tested with one or more *Candida albicans* cells having a mutation in a nucleic acid molecule corresponding to the sequences according to any of claims 1 to 8 which mutation results in overexpression or underexpression of said polypeptides, in addition to contacting one or more wild type *Candida albicans* cells with said compound,

15 (b) monitoring the growth and/or activity of said mutated cell compared to said wild type; wherein differential growth or activity of said one or more mutated *Candida* cells is indicative of selective action of said compound on a polypeptide or another polypeptide in the same or a parallel pathway.

20

25

25. A compound identifiable according to the method of claim 24.

30 26. A compound according to claim 25 for use as a medicament.

27. Use of a compound according to claim 25 in the preparation of a medicament for treating *Candida albicans* associated diseases.

35

28. A pharmaceutical composition comprising a

- 59 -

compound according to claim 24 together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

5 29. A method of identifying DNA sequences from a cell or organism which DNA encodes polypeptides which are critical for growth or survival of said cell or organism, which method comprises:

10 (a) preparing a cDNA or genomic library from said cell or organism in a suitable expression vector which vector is such that it can either integrate into the genome in said cell or that it permits transcription of antisense RNA from the nucleotide sequences in said
15 cDNA or genomic library,

 (b) selecting transformants exhibiting impaired growth and determining the nucleotide sequence of the cDNA or genomic sequence from the library included in the vector from said
20 transformant.

30. A method according to claim 29 wherein said cell or organism is a yeast or filamentous fungi.

25 31. A method according to claim 29 or 30 wherein said cell or organism is any of *Saccharomyces cerevisiae*, *Saccharomyces pombe* or *Candida albicans*.

30 32. Plasmid pGAL1PSiST-1 having the sequence of nucleotides illustrated in Figure 8.

33. Plasmid pGAL1PNiST-1 having the sequence of nucleotides illustrated in Figure 7.

35 34. An antibody capable of binding to a polypeptide according to any of claims 11 to 14.

- 60 -

35. An oligonucleotide comprising a fragment of from 10 to 50 contiguous nucleic acid sequences of a nucleic acid molecule according to any of claims 1 to 10.

5

36. A nucleic acid molecule encoding a polypeptide which is critical for survival and growth of the yeast *Candida albicans*, said nucleic acid molecule comprising the sequences of any of the nucleotide sequences illustrated in Figures 9 to 13.

10

37. A polypeptide which is critical for survival and growth of the yeast *Candida albicans*, said polypeptide comprising the amino acid sequences of any of the sequences illustrated in Figures 14 or 15.

15

38. A method of identifying for the presence of *Candida albicans* in a subject, which method comprises contacting a sample to be tested with nucleic acid molecule according to claim 10 or an antibody according to claim 34, and monitoring for any hybridisation with said molecule or binding to said antibody.

20

39. A kit for monitoring *Candida albicans* infection comprising a molecule according to claim 9 or 10, or an antibody according to claim 34, and means for contacting said molecule or said antibody with a sample to be tested.

25

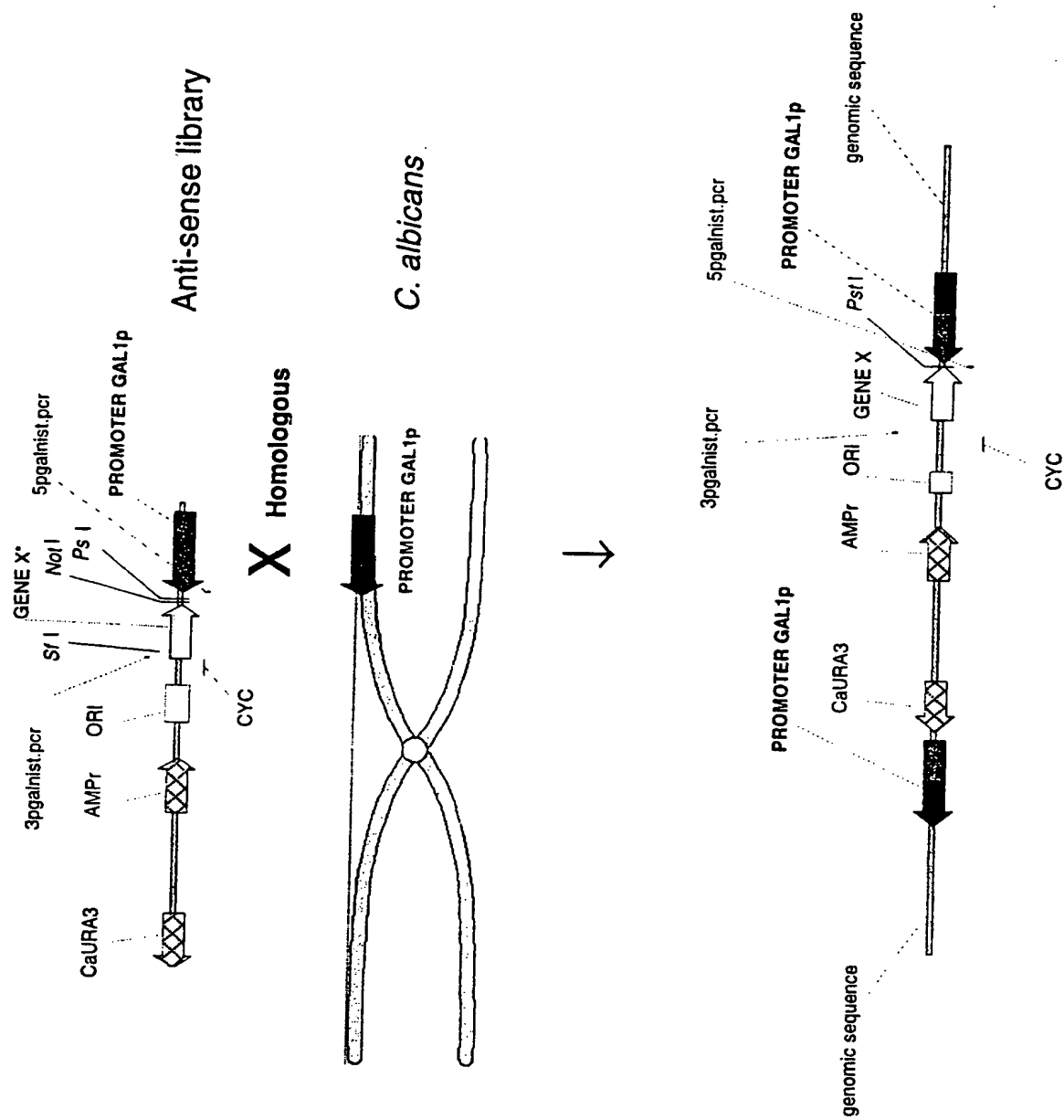
40. A nucleic acid molecule encoding a polypeptide which is critical for survival and growth of the yeast *Candida albicans* and which nucleic acid molecule comprises any of the sequences of nucleotides in Sequence ID Numbers 18, 21, 29, 31, 33, 44, 76, 80 and the sequences identified in Figures 9 and 13.

30

35

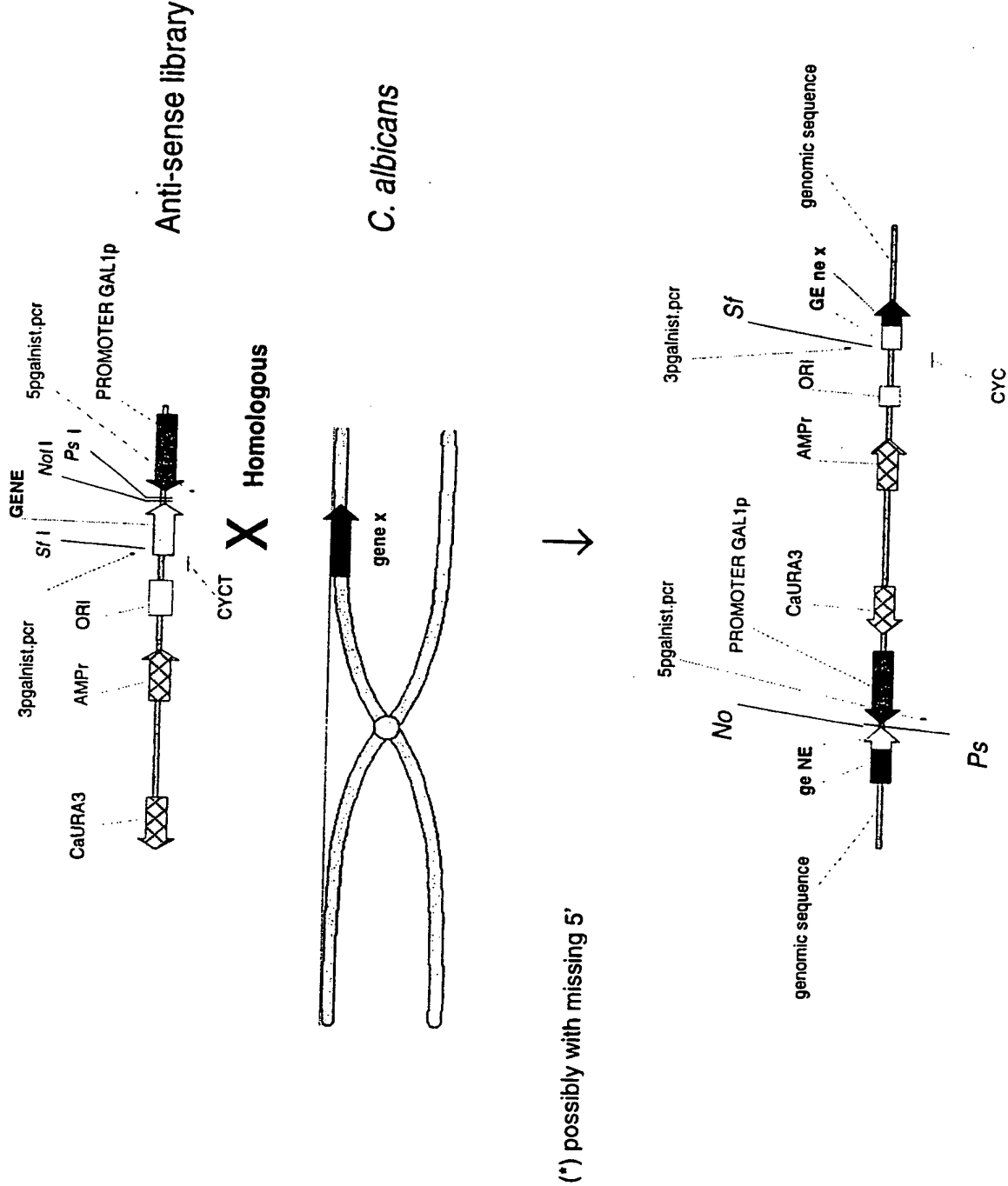
1/63

Figure 1A:



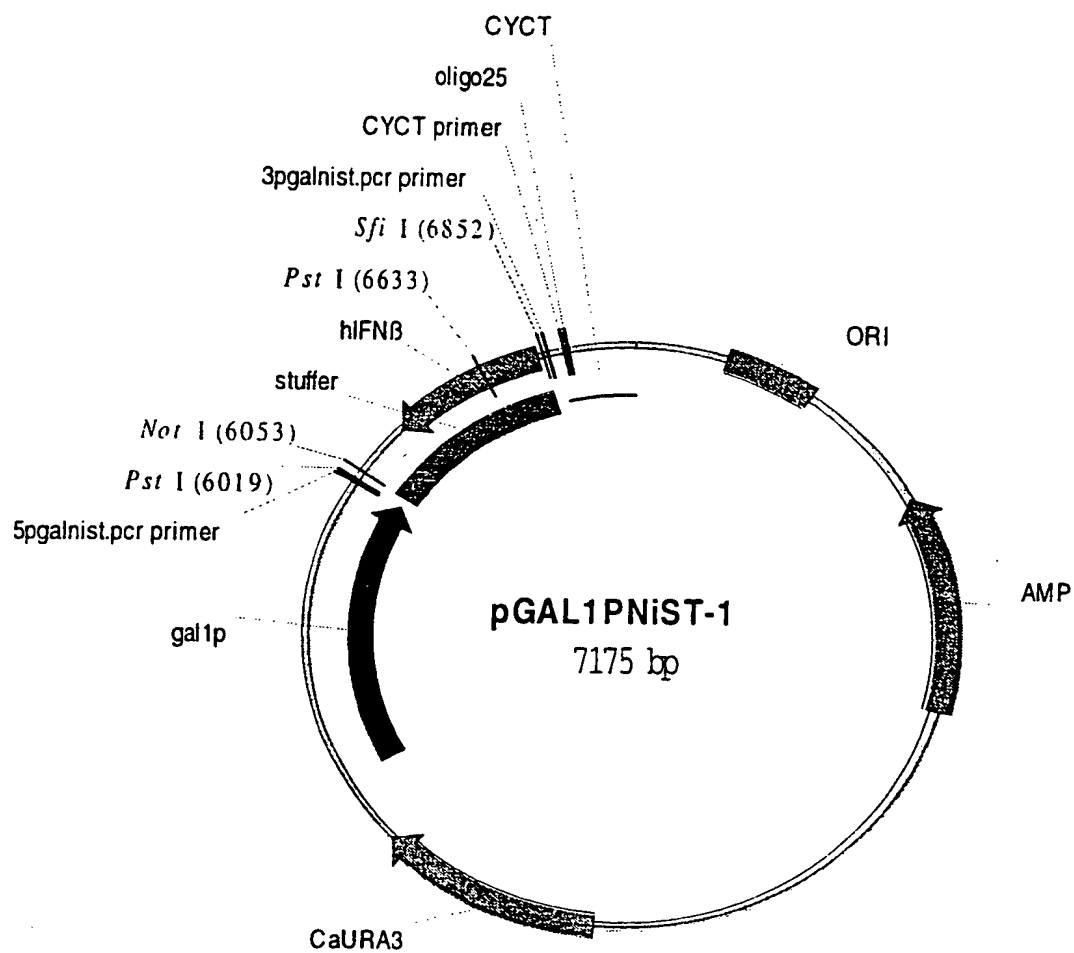
2/63

Figure 1B:



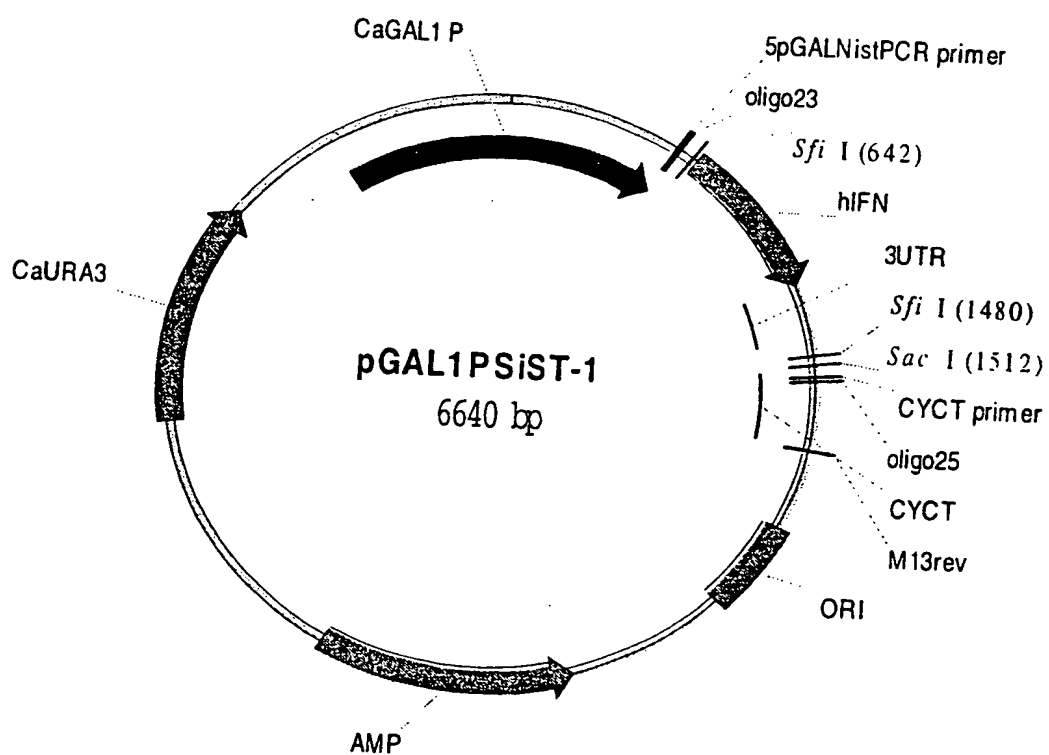
3/63

FIG. 2(a)



4/63

FIG. 2(b)



5/63

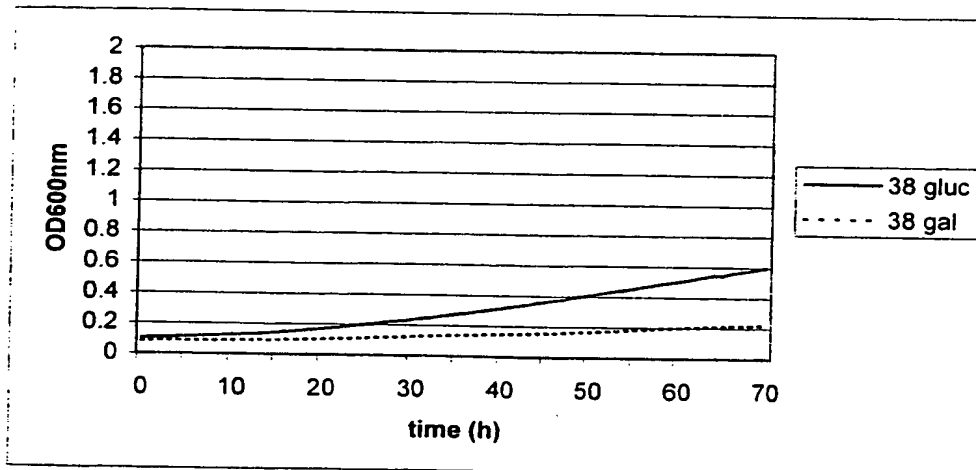
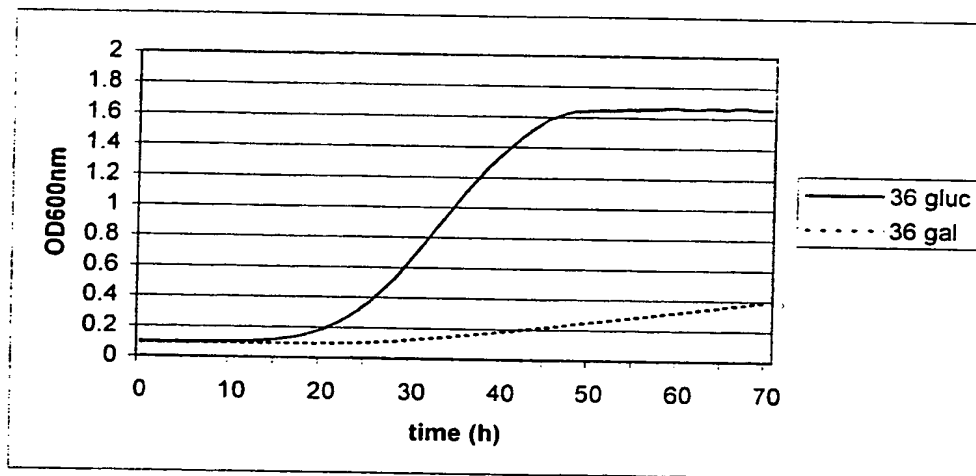
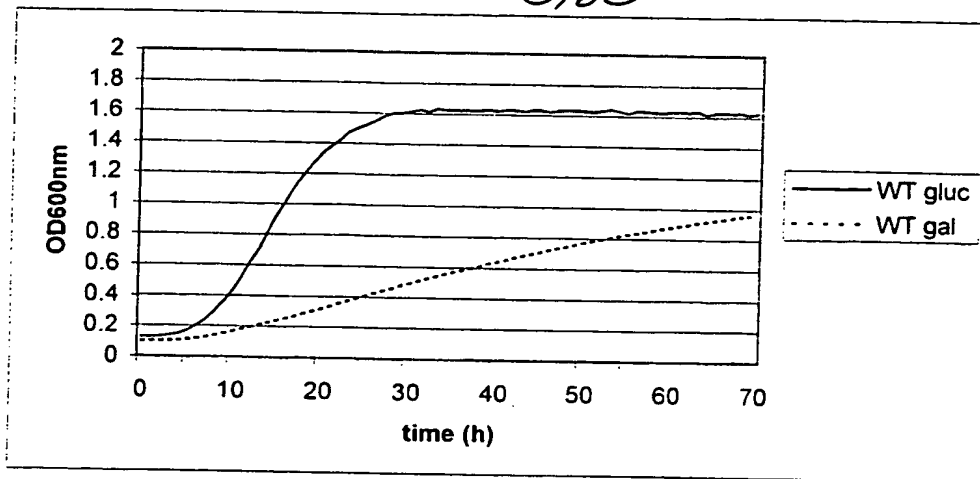


FIG. 3.

6/63

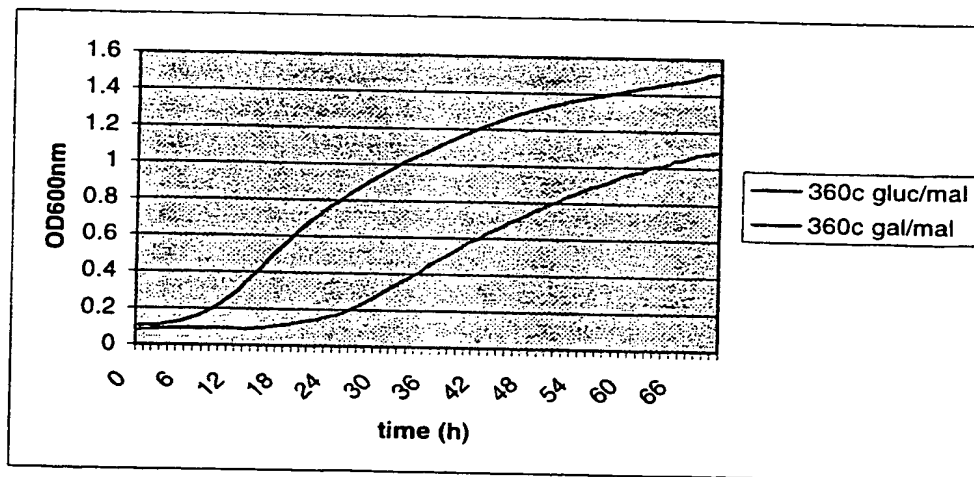
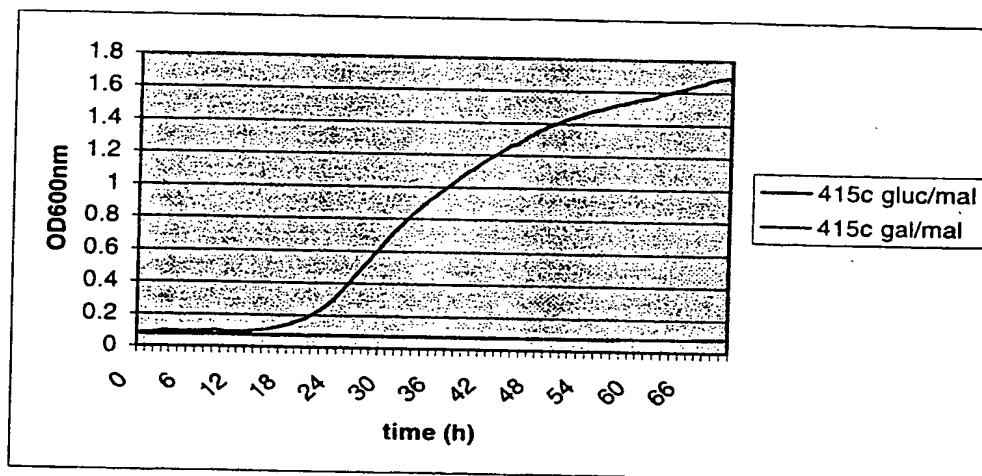
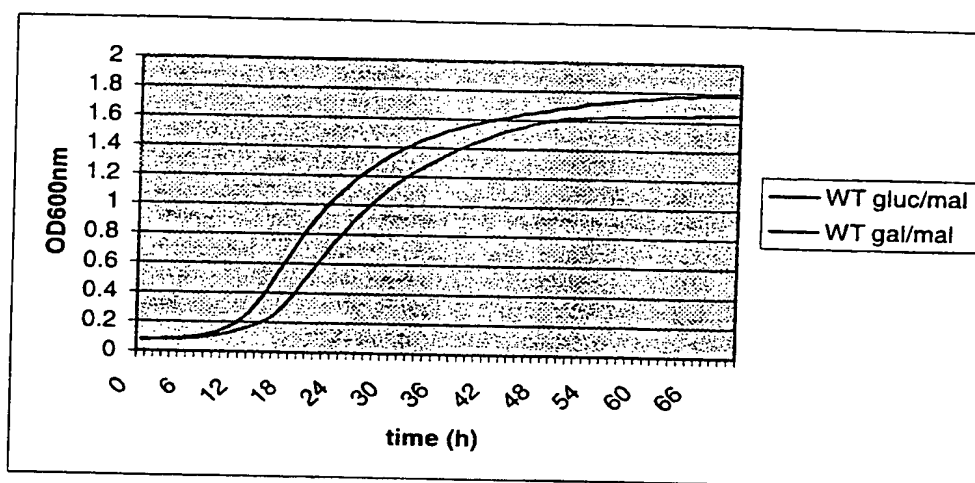
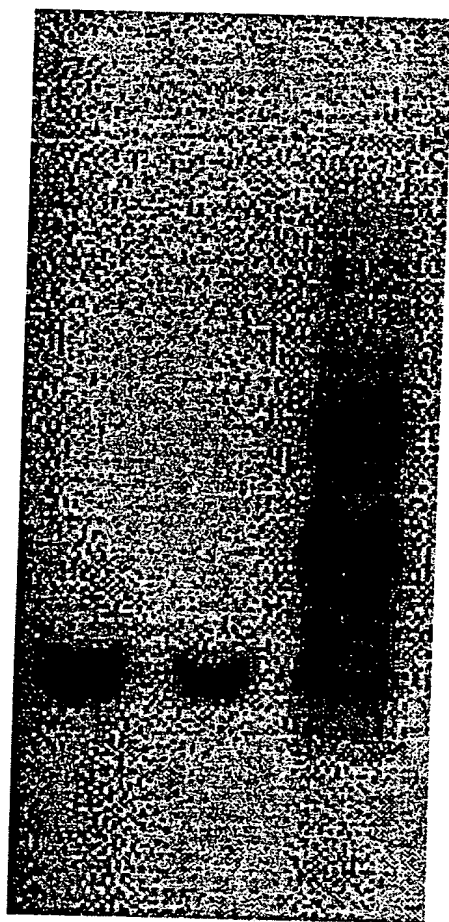


FIG. 3 (CONTINUED)

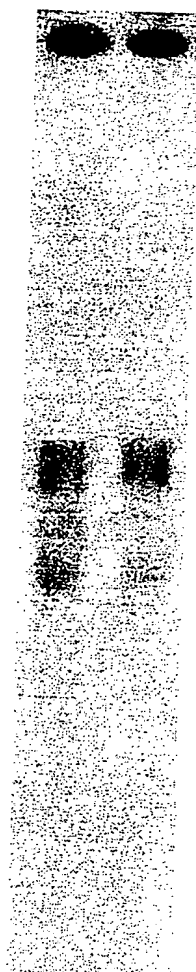
8/63

Figure 5:



9/63

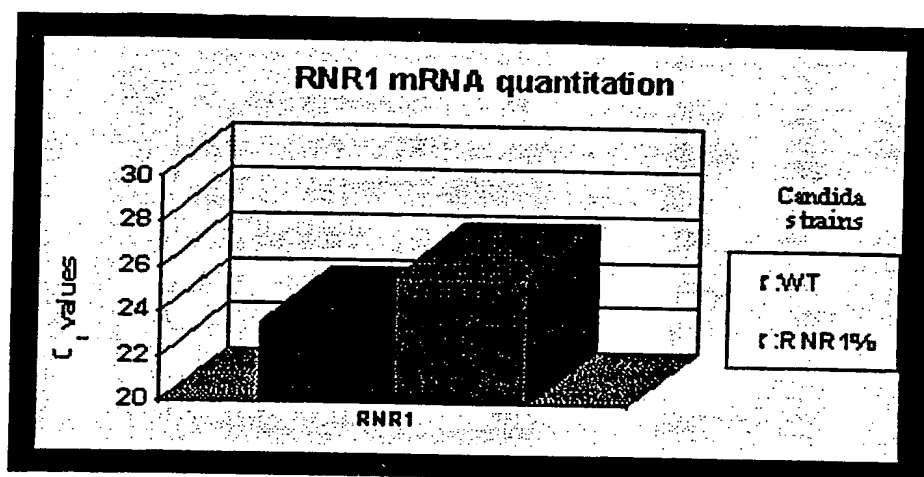
Figure 6A



1: RNF11 mutant
2: Wild type

10/63

Figure 6B



11/63

FIG. 7

HindIII

1 AGCTTGAGTA TTCTATAGTG TCACCTAAAT AGCTTGCGGT AATCATGGTC
TCGAACATCAT AAGATATCAC AGTGGATTTA TCGAACCGCA TTAGTACCAG
.....
51 ATAGCTGTTT CCTGTGTGAA ATTGTTATCC GTCACAATT CCACACAACA
TATCGACAAA GGACACACTT TAACAATAGG CGAGTGTTAA GGTGTGTTGT
.....
101 TACGAGCCCG AAGCATAAAG TGTAAGCCT GGGGTGCCTA ATGAGTGAGC
ATGCTCGGCC TTCGTATTTC ACATTTCGGA CCCCACGGAT TACTCACTCG
.....
151 TAACTCACAT TAATTGCGTT GCGCTCACTG CCCGCTTTCC AGTCGGGAAA
ATTGAGTGTA ATTAACGCAA CGCGAGTGAC GGGCGAAAGG TCAGCCCTTT
.....
201 CCTGTCGTGC CAGCTGCATT AATGAATCGG CCAACGCGCG GGGAGAGGCG
GGACAGCAGG GTCGACGTAA TACTTAGCC GGTTCGCGCG CCCTCTCCGC
.....
251 GTTTGCGTAT TGGGCGCTCT TCCGCTTCCT CGCTCACTGA CTCGCTGCGC
CAAACGCATA ACCCGCGAGA AGCGAAGGA GCGAGTGAAT GAGCGACGCG
.....
301 TCGGTCGTTT GGCTGCGGCG AGCGGTATCA GCTCACTCAA AGGCGGTAAT
AGCCAGCAAG CCGACGCGCG TCGCCATAGT CGAGTGAGTT TCCGCCATTA
.....
351 ACGGTTATCC ACAGAATCAG GGGATAACGC AGGAAAGAAC ATGTGAGCAA
TGCCAAATAGG TGTCTTAGTC CCTATTGCG TCCTTTCTTG TACACTCGTT
.....
401 AAGGCCAGCA AAAGGCCAGG AACCGTAAAA AGGCCGCGTT GCTGGCGTTT
TTCCGGTCTG TTTCCGGTCC TTGGCATTTC TCCGCGCAA CGACCGCAA
.....
451 TTCCATAGGC TCCGCCCCC TCACGAGCAT CACAAAAATC GACGCTCAAG
AAGGTATCCG AGGCGGGGGG ACTGCTCGTA GTGTTTTTAG CTGCGAGTTC
.....
501 TCAGAGGTGG CGAAACCCGA CAGGACTATA AAGATACCAG GCGTTTCCCC
AGTCTCCACC GCTTTGGGCT GTCCTGATAT TTCTATGGTC CGAAAGGGG
.....
551 CTGGAAGCTC CCTCGTGCGC TCTCCTGTTT CGACCTTGCC GCTTACCGGA
GACCTTCGAG GGAGCACGCG AGAGGACAAG GCTGGGACGG CGAATGGCCT
.....
601 TACCTGTCCG CCTTTCTCCC TTCGGGAAGC GTGGCGCTTT CTCATAGCTC
ATGGACAGGC GGAAAGAGGG AAGCCCTTCG CACCGCGAAA GAGTATCGAG
.....
651 ACGCTGTAGG TATCTCAGTT CCGTGTAAGT CGTTCGCTCC AAGCTGGGCT
TGCGACATCC ATAGAGTCAA GCCACATCCA GCAAGCGAGG TTCGACCCGA
.....

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701 GTGTGCACGA ACCCCCCGTT CAGCCCGACC GCTGCGCCTT ATCCGGTAAC
CACACGTGCT TGGGGGGCAA GTCGGGCTGG CGACGCGGAA TAGGCCATTG
.....
751 TATCGTCTTG AGTCCAACCC GGTAAAGACAC GACTTATCGC CACTGGCAGC
ATAGCAGAAC TCAGGTGGG CCAATCTGTG CTGAATAGCG GTGACCGTCG
.....
801 AGCCACTGGT AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG
TCGGTGACCA TTGTCTAAT CTTCTCGCTC CATACATCCG CCACGATGC
.....
851 AGTTCTTGAA GTGGTGGCCT AACTACGGCT AACTAGAAG GACAGTATTT
TCAAGAACTT CACCACCGGA TTGATGCCGA TGTGATCTTC CTGTCATAAA
.....
901 GGTATCTGCG CTCTGCTGAA GCGAGTTACC TTCGGAAAAA GAGTTGGTAG
CCATAGACGC GAGACGACTT CCGTCAATGG AAGCCTTTTT CTCAACCATC
.....

12/63

FIG. 7 (CONTINUED)

951 CTCTTGATCC GGCAAACAAA CCACCGCTGG TAGCGGTGGT TTTTTTGTTT
GAGAACTAGG CCGTTTGTTT GGTGGCGACC ATCGCCACCA AAAAAACAAA
.....
1001 GCAAGCAGCA GATTACGCGC AGAAAAAAG GATCTCAAGA AGATCCTTTG
CGTTCGTCGT CTAATGCGCG TCTTTTTTTC CTAGAGTTCT TCTAGGAAAC
.....
1051 ATCTTTTCTA CGGGGTCTGA CGCTCAGTGG AACGAAACT CACGTTAAGG
TAGAAAAGAT GCCCCAGACT GCGAGTCACC TTGCTTTTGA GTGCAATTCC
.....
1101 GATTTTGGTC ATGAGATTAT CAAAAAGGAT CTTACCTAG ATCCTTTTAA
CTAAAACCAG TACTCTAATA GTTTTCCTA GAAGTGGATC TAGGAAAATT
.....
1151 ATTAAAAATG AAGTTTAAA TCAATCTAAA GTATATATGA GTAAACTTGG
TAATTTTAC TTCAAAATTT AGTTAGATTT CATATATACT CATTTGAACC
.....
1201 TCTGACAGTT ACCAATGCTT AATCAGTGAG GCACCTATCT CAGCGATCTG
AGACTGTCAA TGGTTACGAA TTAGTCACTC CGTGGATAGA GTCGCTAGAC
.....
1251 TCTATTTCTG TCATCCATAG TTGCCTGACT CCCCGTCGTG TAGATAACTA
AGATAAAGCA AGTAGGTATC AACGGACTGA GGGGCAGCAC ATCTATTGAT
.....
1301 CGATACGGGA GGGCTTACCA TCTGGCCCCA GTGCTGCAAT GATACCGCGA
GCTATGCCCT CCCGAATGGT AGACCGGGT CACGACGTTA CTATGGCGCT
.....
1351 GACCCACGCT CACCGGCTCC AGATTATCA GCAATAAACC AGCCAGCCGG
CTGGGTGCGA GTGGCCGAGG TCTAAATAGT CGTTATTGG TCGGTGCGCC
.....
1401 AAGGGCCGAG CGCAGAAGTG GTCCTGCAAC TTTATCCGCC TCCATCCAGT
TTCCCGGCTC GCGTCTTAC CAGGACGTTG AAATAGCGG AGGTAGGTCA
.....
1451 CTATTAAATG TTGCCGGGAA GCTAGAGTAA GTAGTTCGCC AGTTAATAGT
GATAATTAAC AACGGCCCTT CGATCTCATT CATCAAGCGG TCAATTATCA
.....
1501 TTGCGCAACG TTGTTGCCAT TGCTACAGGC ATCGTGGTGT CACGCTCGTC
AACGCGTTGC AACAAACGTA ACGATGTCCG TAGCACCACA GTGCGAGCAG
.....
1551 GTTTGGTATG GCTTCATTCA GCTCCGGTTC CCAACGATCA AGGCGAGTTA
CAAACCATAC CGAAGTAAGT CGAGGCCAAG GGTGCTAGT TCCGCTCAAT
.....
1601 CATGATCCCC CATGTTGTGC AAAAAAGCGG TTAGCTCCTT CGGTCCTCCG
GTACTAGGGG GTACAACACG TTTTTCGCC AATCGAGGAA GCCAGGAGGC
.....
1651 ATCGTTGTCA GAAGTAAGTT GGCCGCAAGT TTATCACTCA TGGTTATGGC
TAGCAACAGT CTTCAATCAA CCGGCGTCAC AATAGTGAGT ACCAATACCG
.....
1701 AGCACTGCAT AATTCTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTCTG
TCGTGACGTA TTAAGAGAAAT GACAGTACGG TAGGCATTCT ACGAAAAGAC
.....
1751 TGACTGGTGA GTACTCAACC AAGTCATTCT GAGAATAGTG TATGCGGCGA
ACTGACCACT CATGAGTTGG TTAGTAAGA CTCTTATCAC ATACGCCGCT
.....
1801 CCGAGTTGCT CTTGCCCCGC GTCAATACCG GATAATACCG CGCCACATAG
GGCTCAACGA GAACGGGCGG CAGTTATGCC CTATTATGGC GCGGTGTATC
.....
1851 CAGAAGTTTA AAAGTGCTCA TCATTGAAA ACGTTCTTCG GGGCGAAAAC
GTCTTGAAAT TTTCACGAGT AATAACCTT TGCAAGAAGC CCCGCTTTG
.....

FIG. 7. (CONTINUED) 13/63

ApaLI

1901 TCTCAAGGAT CTTACCGCTG TTGAGATCCA GTTCGATGTA ACCCACTCGT
AGAGTTCTTA GAATGGCGAC AACTCTAGGT CAAGCTACAT TGGGTGAGCA

.....
ApaLI

1951 GCACCCAACCT GATCTTCAGC ATCTTTTACT TTCACCAGCG TTTCTGGGTG
CGTGGGTGTA CTAGAAGTCG TAGAAAATGA AAGTGGTCGC AAAGACCCAC

2001 AGCAAAAACA GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC
TCGTTTTTGT CCTTCGTTT TACGGCGTTT TTTCCCTTAT TCCCGCTGTG

2051 GGAAATGTTG AATACTCATA CTCTTCCTTT TTCAATATTA TTGAAGCATT
CCTTTACAAC TTATGAGTAT GAGAAGGAAA AAGTTATAAT AACTTCGTAA

2101 TATCAGGGTT ATTGTCTCAT GAGCGGATAC ATATTTGAAT GTATTTAGAA
ATAGTCCCAA TAACAGAGTA CTCGCCTATG TATAAACTTA CATAAATCTT

2151 AAATAAACAA ATAGGGGTTT CGCGCACATT TCCCGAAAA GTGCCACCTG
TTTATTTGTT TATCCCAAG GCGCGTGTA AGGGGCTTT CACGGTGGAC

2201 ACGTCTAAGA AACCATTATT ATCATGACAT TAACCTATAA AAATAGGCGT
TGCAGATTCT TTGGTAATAA TAGTACTGTA ATTGGATATT TTTATCCGCA

2251 ATCAGGAGGC CCTTTCGTCT CGCGCGTTTC GGTGATGACG GTGAAAACCT
TAGTGCTCCG GGAAAGCAGA GCGCGCAAAG CCACTACTGC CACTTTTGA

2301 CTGACACATG CAGCTCCCGG AGACGGTCAC AGCTTGCTCG TAAGCGGATG
GACTGTGTAC GTCGAGGGCC TCTGCCAGTG TCGAACAGAC ATTCCGCTAC

2351 CCGGGAGCAG ACAAGCCCGT CAGGGCGCGT CAGCGGGTGT TGGCGGGTGT
GGCCCTCGTC TGTTCGGGCA GTCCCGCGCA GTCGCCCAACA ACCGCCACA

.....
ApaLI

2401 CGGGGCTGGC TTAACATATG GGCATCAGAG CAGATTGTAC TGAGAGTGCA
GCCCCGACCG AATTGATACG CCGTAGTCTC GTCTAACATG ACTCTCACGT

.....
ApaLI

2451 CCATATGCGG TGTGAAATAC CGCACAGATG CGTAAGGAGA AAATACCGCA
GGTATACGCC AACTTTATG GCGTGTCTAC GCATTCTCT TTTATGGCGT

2501 TCAGGCGAAA TTGTAAACGT TAATATTTTG TTAAATTCG CGTTAAATAT
AGTCCGCTTT AACATTTGCA ATTATAAAC AATTTTAAGC GCAATTTATA

2551 TTGTTAAATC AGCTCATTTT TTAACCAATA GGCCGAAATC GGCAAAATCC
AACAATTTAG TCGAGTAAA AATTGGTTAT CCGGCTTTAG CCGTTTATAG

2601 CTTATAAATC AAAAGAATAG ACCGAGATAG GGTGAGTGT TGTTCAGTT
GAATATTTAG TTTTCTTATC TGGCTCTATC CCAACTCACA ACAAGGTCAA

2651 TGGAACAAGA GTCCACTATT AAAGAACGTG GACTCCAACG TCAAAGGGCG
ACCTTGTTCT CAGGTGATAA TTTCTTGCAC CTGAGGTTGC AGTTCCCGC

2701 AAAAACCGTC TATCAGGGCG ATGGCCCACT ACGTGAACCA TCACCCAAAT
TTTTTGGCAG ATAGTCCCGC TACCGGGTGA TGCACCTGGT AGTGGGTTTA

2751 CAAGTTTTTT GCGGTCGAGG TCCCGTAAAG CTCTAAATCG GAACCCTAAA
GTTCAAAAA CGCCAGCTCC ACGGCATTTC GAGATTTAGC CTGGGATTT

14/63

FIG. 7. (CONTINUED)

2801 GGGAGCCCC GATTAGAGC TTGACGGGGA AAGCCGGCGA ACGTGGCGAG
 CCTCGGGGG CTAAATCTCG AACTGCCCCCT TTCGGCCGCT TGCACCGCTC

 2851 AAAGGAAGGG AAGAAAGCGA AAGGAGCGGG CGCTAGGGCG CTGGCAAGTG
 TTTCCTTCCC TTCTTCGCT TTCCTCGCCC GCGATCCCGC GACCGTTCAC

 2901 TAGCGGTCAC GCTGCGCGTA ACCACCACAC CCGCCGCGCT TAATGCGCG
 ATCGCCAGTG CGACGCGCAT TGGTGGTGTG GCGGCGCGA ATTACGCGG

 2951 CTACAGGGCG CGTCCATTCC CCATTACGGC TGCGCAACTG TTGGGAAGGG
 GATGTCCCGC GCAGGTAAGC CGTAAGTCCG ACGCGTTGAC AACCTTCCC

 3001 CGATCGGTGC GGGCTCTTC GCTATTACGC CAGCTGGCGA AAGGGGGATG
 GCTAGCCACG CCCGAGAAG CGATAATGCG GTCGACCGCT TCCCCCTAC

 3051 TGCTGCAAGG CGATTAAGTT GGGTAACGCC AGGGTTTTCC CAGTCACGAC
 ACGACGTTCC GCTAATTCAA CCCATTGCGG TCCCAAAAGG GTCAGTGCTG

 3101 GTTGTAAGAC GACGGCCAGT GAATTGTAAT ACGACTCACT ATAGGGCGAA
 CAACATTTTG CTGCCGCTCA CTTAACATTA TGCTGAGTGA TATCCCGCTT

 3151 TTGGTTTTCC AATGATGAGC ACTTTTAAAG TTCTGCTATG TGGCGCGTA
 AACCAAAAGG TTACTACTCG TGAAAATTTC AAGACGATAC ACCGCGCCAT

 3201 TTATCCCGTG TTGACGCCGG GCAAGAGCAA CTCGGTCGCC GCATACACTA
 AATAGGGCAC AACTGCGGCC CGTCTCGTT GAGCCAGCGG CGTATGTGAT

 3251 TTCTCAGAAT GACTTGGTGG AGTACTAATA GGAATTGATT TGGATGGTAT
 AAGAGTCTTA CTGAACCAAC TCATGATTAT CCTTAACTAA ACCTACCATA

 3301 AAACGGAAAC AAAAAAAGA GCTGGTACTA CTTCTTTTAA AATTATTTTA
 TTTCCTTTG TTTTCTTCT CGACCATGAT GAAAGAAATT TTAATAAAAT

 3351 TTATTTGATT TTATTTAATA GTATATATTA TATTTTGAAC GTAGATTATT
 AATAAACTAA AATAAATTAT CATATATAAT ATAAAACTTG CATCTAATAA

 3401 TTGTTGAAAG TGCTGTAGT GCCATTGATT CGTAACACTA ATTCTGTATT
 AACAACTTTC AACGACATCA CGGTAACATA GCATTGTGAT TAAGACATAA

 3451 AGTCATTCTT CTGTTTGAT AGTATCCAAA AAAACGGCTA TTTTGTGCA
 TCAGTAAGGA GAACAACTA TCATAGGTTT TTTTGCCGAT AAAAAACGT

 3501 ATCTTATTTT CTGCATATTA TACAGATAAC ATAATGAAAG AAAAAATCTT
 TAGAATAAAG GACGTATAAT ATGTCTATTG TATTACTTTC TTTTGTAGAA

 3551 TTTTGTGTT CTTCATGAT GATTCAACC ATTCTTTTAA ACATTGATCA
 AAAAAACAA GAAGTACTA CTAAAGTTGG TAAGAAAATT TGTAAGTAGT

 3601 ATTCCTGAGC AACACCCCA TACACACTGG TTTATATACC GCCCCTTTAA
 TAAGGACTCG TTGTGGGGT AAGTGTGACC AAATATATGG CGGGGAAAT

 3651 CAGTTGAAGA AAGAAATAGA AATAGAAATA GCAAACAAA GATATGACAG
 GTCAACTTCT TTCTTATCT TTATCTTTAT CGTTGTTTT CTATACTGTC

 3701 TCAACACTAA GACCTATAGT GAGAGAGCAG AAACATCATG CTCACCAGTA
 AGTTGTGATT CTGGATATCA CTCTCTCGTC TTTGAGTACG GAGTGGTCAT

 3751 GCACAGCGAT TATTTGATT AATGGAAGT AAGAAAACCA ATTTATGTGC
 CGTGTGCTA ATAAAGCTAA TTACCTTGAC TTCTTTTGGT TAAATACAG

15/63

FIG. 7. (CONTINUED)

EcoRI

3801 ATCAATTGAC GTTGATACCA CTAAGGAATT CCTTGAATTA ATTGATAAAT
TAGTTAACTG CAACTATGGT GATTCCTTAA GGAACCTAAT TAACTATTTA
.....

3851 TAGGTCCTTA TGTATGCTTA ATCAAGACTC ATATTGATAT AATCAATGAT
ATCCAGGAAT ACATACGAAT TAGTTCTGAG TATAACTATA TTAGTTACTA
.....

3901 TTTTCCTATG AATCCACTAT TGAACCATT TTAGAACTTT CACGTAAACA
AAAAGGATAC TTAGGTGATA ACTTGGTAAT AATCTTGAAA GTGCATTGT
.....

3951 TCAATTTATG ATTTTGAAG ATAGAAAATT TGCTGATATT GGTAATACCG
AGTTAAATAC TAAAACTTC TATCTTTTAA ACGACTATAA CCATTATGGC
.....

4001 TAAAGAAACA ATATATTGGT GGAGTTTATA AAATTAGTAG TTGGGCAGAT
ATTCTTTTGT TATATAACCA CCTCAAATAT TTTAATCATC AACCCGTCTA
.....

4051 ATTACCAATG CTCATGGTGT CACTGGGAAT GGAGTGGTTG AAGGATTAAA
TAATGGTTAC GAGTACCACA GTGACCCTTA CCTCACCAAC TTCCTAATTT
.....

4101 ACAGGGAGCT AAAGAAACCA CCACCAACCA AGAGCCAAGA GGGTTATTGA
TGTCCCTCGA TTTCTTTGGT GGTGGTTGGT TCTCGGTTCT CCAATAACT
.....

4151 TGTTAGCTGA ATTATCATCA GTGGGATCAT TAGCATATGG AGAATATTCT
ACAATCGACT TAATAGTAGT CACCCTAGTA ATCGTATACC TCTTATAAGA
.....

4201 CAAAAAAGTG TTGAAATTGC TAAATCCGAT AAGGAATTTG TTATTGGATT
GTTTTGTGAC AACTTTAAGG ATTTAGGCTA TTCCTTAAAC AATAACCTAA
.....

4251 TATTGCCCAA CGTGATATGG GTGGCCAAGA AGAAGGATTT GATTGGCTTA
ATAACGGGTT GCACTATACC CACCGGTTCT TCTTCCTAAA CTAACCGAAT
.....

4301 TTATGACACC TGGAGTTGGA TTAGATGATA AAGGTGATGG ATTAGGACAA
AATACTGTGG ACCTCAACCT AATCTACTAT TCCACTACC TAATCCTGTT
.....

4351 CAATATAGAA CTGTTGATGA AGTTGTTAGC ACTGGAAGTG ATATTATCAT
GTTATATCTT GACAACTACT TCAACAATCG TGACCTTGAC TATAATAGTA
.....

4401 TGTGGTAGA GGATTGTTG GTAAAGGAAG AGATCCAGAT ATTGAAGGTA
ACAACCATCT CTAACAAAC CATTTCCTTC TCTAGGTCTA TAACTTCCAT
.....

4451 AAAGGTATAG AAATGCTGGT TGAATGCTT ATTTGAAAAA GACTGGCCAA
TTTCCATATC TTACGACCA ACCTTACGAA TAACTTTTT CTGACCGGTT
.....

4501 TTATAAATGT GAAGGGGGAG ATTTTCACTT TATTAGATTT GTATATATGT
AATATTTTACA CTTCCCCCTC TAAAAGTGAA ATAATCTAAA CATATATACA
.....

4551 AGAATAAATA AATAAATAAG TTAATAAAT AATTAAATAA GGGTGGTAAT
TCTTATTAT TTATTATTTC AATTATTAT TTAATTTATT CCCACCATTA
.....

4601 TATTACTATT TACAATCAAA GTGGTCTCT CTAGCTGTAA TCCGGGCAGC
ATAATGATAA ATGTTAGTTT CACCCAGGAA GATCGACATT AGGCCCGTCG
.....

4651 GCAACGGAAC ATTCATCAGT GTAAAAATGG AATCAATAAA GCCCTGCGCA
CGTTGCCTTG TAAGTAGTCA CATTTTACC TTAGTTATTT CGGGACGCGT
.....

4701 GCGCGCAGGG TCAGCCTGAA TACGCGTTTA ATGACCAGCA CAGTCGTGAT
CGCGCGTCCC AGTCGGACTT ATGCGCAAAT TACTGGTCTG GTCAGCACTA
.....

16/63
FIG. 7 (CONTINUED)

4751 GGCAAGGTCA GAATAGCCCA AGTCGGCCGA GGGGCCTGTA CAGTGAGGGA
CCGTTCCAGT CTTATCGGGT TCAGCCGGCT CCCC GGACAT GTCACTCCCT
.....

4801 AGATCTGATA TTGACGAAGA GGAACCAATG TAACGTTACA CTGAAGAAAA
TCTAGACTAT AACTGCTTCT CTTGGTTAC ATTGCAATGT GACTTCTTTT
.....

4851 CACACAATAA ACGGGAAGAA ACGGTGTAAA AGTGTGAAAA TAATTTTGA
GTGTGTTATT TGCCCTTCTT TGCCACATT TCACACTTTT ATTAAAACT
.....

4901 ATATCATTTT CTTGGTTTA ATTCCAAACG AAACGTGTTT TTTTAGAGA
TATAGTAAAG GGAACCAAAT TAAGGTTTGC TTTGCACAAA AAAAACTCT
.....

EcoRI

4951 ATGGGAATTC TTATTGGATG TCTAGATTGT TTGTTTACTC CAGACTGTGC
TACCCTTAAG AATAACCTAC AGATCTAACA AACAAATGAG GTCTGACACG
.....

ApaLI

5001 ACAAAAACGT TTGGATGGAT GATCAGAAGA TATTTTATAG CTTAGCTCTA
TGTTTTTGCA AACCTACCTA CTAGTCTTCT ATAAAAATCC GAATCGAGAT
.....

5051 AATATAAGAA ATGATGCTTG AAAAACCAGA CAGAAATTGA GTTTCAAAAA
TTATATTCTT TACTACGAAC TTTTGGTCT GTCTTTAACT CAAAGTTTTT
.....

5101 TTGGTAATGT GAGGTATTAG TCAACTAACC AAATAACAAT GCAAACCGGT
AACCATTACA CTCCATAATC AGTTGATTGG TTTATTGTTA CGTTGGCCA
.....

5151 TGATACATTT CATTTGAAA ATAATGAAAC TGGAATTGGA TGACCAGCAC
ACTATGTAAA GTAAAACCTT TATTACTTTG ACCTTAACCT ACTGGTCGTG
.....

5201 ACAAACACAT AAAGTAATTA TGGGAATTAG AAGCGAACAT AGAGGAGTAC
TGTTTGTTGA TTCATTAAT ACCCTTAATC TTCGCTTGTA TCTCCTCATG
.....

5251 TTGGCCACGA ACAGAATACA AGTGGGAACA CTATTTTCTC CATTGTTTTA
AACCGGTGCT TGTCTTATGT TCACCCTTGT GATAAAAGAG GTAACAAAAT
.....

5301 GTTCTGTTTT TTTGTCAGCC TAGTTTTGTG CTATGTGTAA AAAATATTGC
CAAGACAAAA AAACAGTCGG ATCAAAACAC GATACACATT TTTTATAACG
.....

HindIII

5351 CAAGAAAAAA AGCTTGTTTT GTGGCCAGTG TCCGAAAAAA ATTTTGGGGA
GTTCTTTTTT TCGAACAAAA CACCGGTCAC AGGCTTTTTT TAAAACCCCT
.....

5401 ATCTTCGGAT TAATTTATGT TTCAATCCA TCGGGGAAAG TGGGGGGGAA
TAGAAGCCTA ATTAAATACA AAGTAAGGT AGCCCCTTTC ACCCCCCCTT
.....

5451 AAAATTTTAA GCAGTTCACA AAACCTTCCA AAAATATAT GGACAAAGAT
TTTTAAATTT CGTCAAGTGT TTTGGAAGGT TTTTATATA CCTGTTTCTA
.....

5501 GATTGTATTT TCCCGACACC AAATCATAA TTAATTATGA GAAAGTTAAA
CTAACATAAA AGGGCTGTGG TTTTAGTATT AATTAATACT CTTTCAATTT
.....

5551 TGTAACGTTA CAATTTATGT TATTTGAAG GTGAAAAGCG ATTTATGATT
ACATTGCAAT GTTAAATACA AATAAACTTC CACTTTTCGC TAAATACTAA
.....

5601 TTTCCGAAAT GAAAATTTTT TTTAGGTTTA TTTTMTTGT CGGGCAAAGA
AAAGGCTTTA CTTTTAAAAA AATCCAAAT AAAAAAACA GCCCGTTTCT
.....

17/63
FIG. 7. (CONTINUED)

EcoRI

5651 AAAACTGAAC AAGGATTATT AAAATTTTGT GTGTTTGTGT GTGTCTGGAG
TTTTGACTTG TTCCTAATAA TTTTAAAAAC CACAAACAAA CACAGACCTC

EcoRI

5701 AATTCATTCC TCTCTCATCT TCACACAATG TTTAGACATC TGACACGATT
TTAAGTAAGG AGAGAGTAGA AGTGTGTTAC AAATCTGTAG ACTGTGCTAA

5751 CATGATAGTT CGGTTTCCGG GGTGGGTGTT TAGTTTTTCGT TTTTCTTTTT
GTACTATCAA GCCAAAGGCC CCAACCACAA ATCAAAGCA AAAAGAAAAA

5801 TTTGGAAAG AATGTTTGTAG CTCATTGGTT TTCTTTCTTC ATTCAATAGT
AAAACCTTTC TTACAAAATC GAGTAACCA AAGAAAGAAG TAAGTTATCA

5851 TTTGAAAGAA TTTGCCCACT TGTATTACA ATCATATAAA ATTAACTTT
AAACTTTCTT AAACGGGTGA ACAATAATGT TAGTATATTT TAATTTGAAA

5901 GATATAAAAT AGAGTTTGAA AGTTTCCAG ATCCTTTTGT ATTCTTTGT
CTATATTTTA TCTCAAACCTT TCAAAGGGTC TAGGAAAAAC TAAAGAAACA

5951 AAATTTTTTT TTCTCCACA TATACACACA TACAAACCGA TTTTATAAG
TTTAAAAAAA AAGAGGGTGT ATATGTGTGT ATGTTTGGCT AAAAATATTC

PstI

AvaI

BamHI

6001 AAAGAGTTAT ACCCTGCAGC TCGACCTCGA GGGATCCGGG CCCTCTAGAT
TTTCTCAATA TGGGACGTCG AGCTGGAGCT CCCTAGGCCG GGGAGATCTA

AvaI

6051 GCGGCCGCTA GGCCTCGAGG GACTTTTGCA CCAAAAATAA TTTATTTTCC
CGCCGGCGAT CCGGAGCTCC CTGAAAACGT GGTTTTTTAT AAATAAAAGG

6101 AAAATAAAAT TTAAATAAAT AAAATAACT CATAATTTAA TAAAAATTC
TTTTATTTTA AATTTATTTA TTTTATTTGA GTATTAAAT ATTTTTAAAG

6151 AAAATCTTCT AGTGTCTTTT CATATGCAGT ACATTAGCCA TCAGTCACTT
TTTTAGAAGA TCACAGGAAA GTATACGTCA TGTAATCGGT AGTCAGTGAA

6201 AAACAGCATC TGCTGGTTGA AGAATGCTTG AAGCAATTGT CCAGTCCCG
TTTGTCTAG ACGACCAACT TCTTACGAAC TTCGTTAACA GGTCAGGTC

6251 AGGCACAGGC TAGGAGATCT TCAGTTTCGG AGGTAACCTG TAAGTCTGTT
TCCGTGTCCG ATCCTCTAGA AGTCAAAGCC TCCATTGGAC ATTCAGACAA

6301 AATGAAGTAA AAGTTCCTTA GGATTTCCAC TCTGACTATG GTCCAGGCAC
TTACTTCATT TTCAAGGAAT CCTAAAGGTG AGACTGATAC CAGGTCCGTG

6351 AGTGACTGTA CTCCTTGGCC TTCAGGTAAT GCAGAATCCT CCCATAATAT
TCACTGACAT GAGGAACCGG AAGTCCATTA CGTCTTAGGA GGGTATTATA

6401 CTTTTCAGGT GCAGACTGCT CATGAGTTT CCCCTGGTGA AATCTTCTTT
GAAAAGTCCA CGTCTGACGA GTACTCAAAA GGGGACCACT TTAGAAGAAA

6451 CTCCAGTTTT TCTTCCAGGA CTGTCTTCAG ATGGTTTATC TGATGATAGA
GAGGTCAAAA AGAAGGTCCT GACAGAAGTC TACCAATAG ACTACTATCT

6501 CATTAGCCAG GAGGTCTCA ACAATAGTCT CATTCCAGCC AGTGCTAGAT
GTAATCGGTC CTCCAAGAGT TGTATCAGA GTAAGGTCGG TCACGATCTA

18/63

FIG. 7. (CONTINUED)

6551 GAATCTTGTC TGAAAATAGC AAAGATGTTT TGGAGCATCT CATAGATGGT
CTTAGAACAG ACTTTTATCG TTTCTACAAG ACCTCGTAGA GTATCTACCA
.....

PstI

6601 CAATGCGGCG TCCTCCTTCT GGAAGTGTCT CAGCTGCTTA ATCTCCTCAG
GTTACGCCGC AGGAGGAAGA CCTTGACGAC GTCGACGAAT TAGAGGAGTC
.....

6651 GGATGTCAAA GTTCATCCTG TCCTTGAGGC AGTATTCAAG CCTCCCATTC
CCTACAGTTT CAAGTAGGAC AGGAACTCCG TCATAAGTTC GGAGGGTAAG
.....

6701 AATTGCCACA GGAGCTTCTG AACTGAAAA TTGCTGCTTC TTTGTAGGAA
TTAACGGTGT CCTCGAAGAC TGTGACTTTT AACGACGAAG AACATCCTT
.....

6751 TCCAAGCAAG TTGTAGCTCA TGGAAAGAGC TGTAGTGGAG AAGCACAACA
AGGTTTCGTT AACATCGAGT ACCTTTCTCG ACATCACCTC TCGTGTGTG
.....

AvaI

6801 GGAGAGCAAT TTGGAGGAGA CACTTGTGTG TCATGTTCTT CGAGGCCTTT
CCTCTCGTTA AACCTCCTCT GTGAACAACC AGTACAAGGA GCTCCGGAAA
.....

BamHI

6851 TTGGCCAGCT GCGCCTGCT GCGCGACGGC GAGCTGCTCA CCACCCAGGA
AACCGGTCGA CCGCGGACGA CGCGCTGCCG CTCGACGAGT GGTGGGTCTT
.....

BamHI

6901 TCCGTCCCCC TTTTCCTTTG TCGATATCAT GTAATTAGTT ATGTCACGCT
AGGCAGGGGG AAAAGGAAAC AGCTATAGTA CATTAAATCAA TACAGTGCGA
.....

6951 TACATTACAG CCTCCCCC ACATCCGCTC TAACCGAAAA GGAAGGAGTT
ATGTAAGTGC GGGAGGGGGG TGTAGGCGAG ATTGGCTTTT CCTTCCTCAA
.....

7001 AGACAACCTG AAGTCTAGG CCTATTAT TTTTATATAG TTATGTTAGT
TCTGTTGGAC TTCAGATCCA GGGATAAATA AAAAAATATC AATACAATCA
.....

7051 ATTAAGAACG TTATTTATAT TCCTAATTTT TCTTTTTTTT CTGTACAGAC
TAATTCCTGC AATAAATATA AAGTTTAAAA AGAAAAAATA GACATGCTG
.....

7101 GCGTGACGC ATGTAACATT AACTGAAAA CCTTGCTTGA GAAGGTTTGT
CGCACATGCG TACATTGTAA TATGACTTTT GGAACGAACT CTTCCAAAAC
.....

HindIII

7151 GGACGCTCGA AGGCTTTAAT TTGCA
CCTGCGAGCT TCCGAAATTA AACGT
.....

19/63
FIG. 8.

```
1  TTCCATCGGG GAAAGTGGG GGGAAAAAAT TTTAAGCAGT TCACAAAACC
   AAGGTAGCCC CTTTCACCCC CCCTTTTTTA AAATTCGTCA AGTGTTTTGG
.....
51  TTCCAAAAAA TATATGGACA AAGATGATTG TATTTTCCCG ACACCAAAAT
   AAGGTTTTTT ATATACCTGT TTCTACTAAC ATAAAAGGGC TGTGGTTTTA
.....
101 CATAATTAAT TATGAGAAAG TTAAATGTAA CGTTACAATT TATGTTTATT
   GTATTAATTA ATACTCTTTC AATTTACATT GCAATGTAA ATACAAATAA
.....
151 TGAAGGTGAA AAGCGATTTA TGATTTTTTC GAAATGAAAA TTTTTTTAG
   ACTTCCACTT TTCGCTAAAT ACTAAAAAGG CTTTACTTTT AAAAAAATC
.....
201 GTTTATTTTT TTTGTCGGGC AAAGAAAAAC TGAACAAGGA TTATTAAAT
   CAAATAAAAA AACAGCCCG TTTCTTTTTG ACTTGTTCTT AATAATTTA
.....
                                EcoRI
                                -----
251 TTTTGGTGTT TGTGTGTGTC TGGAGAATTC ATTCCTCTCT CATCTTCACA
   AAAACCACAA ACAACACAG ACCTCTTAAG TAAGGAGAGA GTAGAAGTGT
.....
301 CAATGTTTAG ACATCTGACA CGATTCATGA TAGTTCGGTT TCCGGGGTTG
   GTTACAAATC TGTAGACTGT GCTAAGTACT ATCAAGCCAA AGGCCCAAC
.....
351 GTGTTTAGTT TTCGTTTTTC TTTTTTTTTG GAAAGAATGT TTAGCTCAT
   CACAAATCAA AAGCAAAAAG AAAAAAAAAC CTTTCTTACA AAATCGAGTA
.....
401 TGGTTTTCTT TCTTCATTCA ATAGTTTTGA AAGAATTTGC CCACTTGTTA
   ACCAAAAGAA AGAAGTAACT TATCAAAACT TTCTTAAACG GGTGAACAAT
.....
451 TTACAATCAT ATAAATTAA ACTTTGATAT AAAATAGAGT TTGAAAGTTT
   AATGTTAGTA TATTTAATT TGAACTATA TTTTATCTCA AACTTTCAAA
.....
501 CCCAGATCCT TTTTGATTTC TTGTAAATT TTTTTTCTC CCACATATAC
   GGGTCTAGGA AAAACTAAAG AAACATTTAA AAAAAAGAG GGTGTATATG
.....
                                PstI
                                -----
551 ACACATACAA ACCGATTTTT ATAAGAAAGA GTTATACCCT GCAGCTCGAC
   TGTGTATGTT TGGCTAAAAA TATTCTTTCT CAATATGGGA CGTCGAGCTG
.....
                                PstI      HindIII      AvaI
                                -----
601 CTCGACTGTT TAAACCTGCA GGCATGCAAG CTTGGCCAAA AAGGCCTCGA
   GAGCTGACAA ATTTGGACGT CCGTACGTTT GAACCGGTTT TTCCGGAGCT
.....
                                AvaI
                                -----
651 GGAACATGAC CAACAAGTGT CTCCTCCAAA TTGCTCTCCT GTTGTGCTTC
   CCTTGTTACTG GTTGTTTACA GAGGAGGTTT AACGAGAGGA CAACACGAAG
.....
701 TCCACTACAG CTCTTCCAT GAGCTACAAC TTGCTTGGAT TCCTACAAAG
   AGGTGATGTC GAGAAAGGTA CTCGATGTTG AACGAACCTA AGGATGTTTC
.....
751 AAGCAGCAAT TTTCAGTGTG AGAAGCTCCT GTGGCAATTG AATGGGAGGC
   TTGTCGTTA AAAGTCACAG TCTTCGAGGA CACCGTTAAC TTACCCTCCG
.....
801 TTGAATACTG CCTCAAGGAC AGGATGAACT TTGACATCCC TGAGGAGATT
   AACTTATGAC GGAGTTCCTG TCTTACTTGA AACTGTAGGG ACTCCTCTAA
.....
```

20/63

FIG. 8. (CONTINUED)

PstI

851 AAGCAGCTGC AGCAGTTCCA GAAGGAGGAC GCCGCATTGA CCATCTATGA
 TCGTCGACG TCGTCAAGGT CTCCTCCTG CGGCGTAACT GGTAGATACT

 901 GATGCTCCAG AACATCTTTG CTATTTTCAG ACAAGATTCA TCTAGCACTG
 CTACGAGGTC TTGTAGAAAC GATAAAAGTC TGTCTAAGT AGATCGTGAC

 951 GCTGGAATGA GACTATTGTT GAGAACCTCC TGGCTAATGT CTATCATCAG
 CGACCTTACT CTGATAACAA CTCTTGAGG ACCGATTACA GATAGTAGTC

 1001 ATAAACCATC TGAAGACAGT CCTGGAAGAA AACTGGAGA AAGAAGATTT
 TATTTGGTAG ACTTCGTCA GGACCTTCTT TTTGACCTCT TTCTTCTAAA

 1051 CACCAGGGGA AACTCATGA GCAGTCTGCA CCTGAAAAGA TATTATGGGA
 GTGGTCCCCT TTGAGTACT CGTCAGACGT GGACTTTTCT ATAATACCTT

 1101 GGATTCTGCA TTACCTGAAG GCCAAGGAGT ACAGTCACTG TGCCTGGACC
 CCTAAGACGT AATGGACTTC CGGTTCTCTCA TGTCAGTGAC ACGGACCTGG

 1151 ATAGTCAGAG TGGAAATCCT AAGGAACTTT TACTTCATTA ACAGACTTAC
 TATCAGTCTC ACCTTTAGGA TTCCTTGAAA ATGAAGTAAT TGTCTGAATG

 1201 AGGTTACCTC CGAAACTGAA GATCTCCTAG CCTGTGCCTC TGGGACTGGA
 TCCAATGGAG GCTTTGACTT CTAGAGGATC GGACACGGAG ACCCTGACCT

 1251 CAATTGCTTC AAGCATTCTT CAACCAGCAG ATGCTGTTTA AGTGACTGAT
 GTTAACGAAG TTCGTAAGAA GTTGGTCGTC TACGACAAAT TCACTGACTA

 1301 GGCTAATGTA CTGCATATGA AAGGACACTA GAAGATTTTG AAATTTTAT
 CCGATTACAT GACGTATACT TTCCTGTGAT CTTCTAAAAC TTTAAAAATA

 1351 TAAATTATGA GTTATTTTAA TTTATTTAAA TTTTATTTTG GAAAATAAAT
 ATTTAATACT CAATAAAAAT AAATAAATTT AAAATAAAAC CTTTATTTTA

XmaI

SmaI

BamHI

AvaI

AvaI

1401 TATTTTGGT GCAAAAGTCC CTCGAGGCCT AGCGGCCGCC TAGAGGATCC
 ATAAAAACCA CGTTTTCAGG GAGCTCCGGA TCGCCGGCGG ATCTCCTAGG

XmaI

SmaI

AvaI

1451 CCGGGCGCTA GGCGGCGCT AGGCCTTTT GGCCAAGCTC GAATTTTCAG
 GGCCCGCGAT CCGCCGGCGA TCCGGAAGAA CCGGTTTCAG CTAAAGCTC

XmaI

SmaI

EcoRI

AvaI

ClaI

1501 GAATTCGAGC TCGGTACCCG GGGGATCGAT CCGTCCCCCT TTCTTTTGT
 CTTAAGCTCG AGCCATGGGC CCCCTAGCTA GGCAGGGGGA AAAGGAAACA

21/63

FIG. 8. (CONTINUED)

1551 CGATATCATG TAATTAGTTA TGTCACGCTT ACATTCACGC CCTCCCCCA
GCTATAGTAC ATTAATCAAT ACAGTGCAGG TGTAAGTGCG GGAGGGGGGT

1601 CATCCGCTCT AACCGAAAAG GAAGGAGTTA GACAACCTGA AGTCTAGGTC
GTAGCGGAGA TTGGCTTTTC CTTCCTCAAT CTGTTGGACT TCAGATCCAG

1651 CCTATTTATT TTTTATAGT TATGTTAGTA TTAAGAACGT TATTTATATT
GGATAAATAA AAAAATATCA ATACAATCAT AATTCCTGCA ATAAATATAA

1701 TCAAATTTTT CTMTTTTTTC TGTACAGACG CGTGTACGCA TGTAACATTA
AGTTTAAAAA GAAAAAAAAG ACATGCTGCG GCACATGCGT ACATTGTAAT

1751 TACTGAAAAC CTTGCTTGAG AAGGTTTTGG GACGCTCGAA GGCTTTAATT
ATGACTTTTG GAACGAACTC TCCAAAACC CTGCGAGCTT CCGAAATTAA

1801 TGCAAGCTAG CTTGGCGTAA TCATGGTCAT AGCTGTTTCC TGTGTGAAT
ACGTTTCGATC GAACCGCATT AGTACCAGTA TCGACAAAGG ACACACTTAA

1851 TGTTATCCGC TCACAATTCC ACACAACATA CGAGCCGGAA GCATAAAGTG
ACAATAGGCG AGTGTTAAGG TGTGTTGTAT GCTCGGCCTT CGTATTTTAC

1901 TAAAGCCTGG GGTGCCTAAT GAGTGAGCTA ACTCACATTA ATTGCGTTGC
ATTTCCGACC CCACGGATTA CTCACTCGAT TGAGTGTAAT TAACGCAACG

1951 GCTCACTGCC CGCTTTCCAG TCGGGAACC TGTCGTGCCA GAGATCTCTG
CGAGTGACGG GCGAAAGGTC AGCCCTTGG ACAGCACGGT CTCTAGAGAC

2001 CATTAAATGAA TCGGCCAAGC CCGGGGAGA GGCGGTTTGC GTATTGGGCG
GTAATTACTT AGCCGGTTGC GCGCCCTCT CCGCCAAACG CATAACCCGC

2051 CTCTCCGCT TCCTCGCTCA CTGACTCGCT GCGCTCGGTC GTTCGGCTGC
GAGAAGGCGA AGGAGCGAGT SACTGAGCGA CGCGAGCCAG CAAGCCGACG

ClaI

2101 GGCGAGCGGT ATCAGATCGA TCTACTCAA AGGCGGTAAT ACGGTTATCC
CCGCTCGCCA TAGTCTAGCT AGAGTGAGTT TCCGCCATTA TGCCAATAGG

2151 ACAGAATCAG GGGATAACGC AGGAAAGAAC ATGTGAGCAA AAGGCCAGCA
TGCTTAGTC CCCTATTGCG TCCCTTCTTG TACACTCGTT TTCCGGTCGT

2201 AAAGGCCAGG AACCGTAAAA AGGCCGCGTT GCTGGCGTTT TTCCATAGGC
TTCCCGGTCC TTGGCATTTT TCCGGCGCAA CGACCGCAA AAGGTATCCG

2251 TCCGCCCCC TGACGAGCAT CACAAAAATC GACGCTCAAG TCAGAGGTGG
AGGCGGGGG ACTGCTCGTA GTGTTTTAG CTGCGAGTTC AGTCTCCACC

2301 CGAAACCCGA CAGGACTATA AGATACCAG GCGTTTCCCC CTGGAAGCTC
GCTTTGGGCT GTCTGATA TCTATGGTC CGCAAAGGGG GACCTTCGAG

2351 CCTCGTGCGC TCTCCTGTTT CACCCCTGCC GCTTACCGGA TACCTGTCCG
GGAGCACCGG AGAGGACAAG CTGGGACGG CGAATGGCCT ATGGACAGGC

2401 CCTTCTCCC TTCGGGAAGC GTGGCGTTT CTCATAGCTC ACGCTGTAGG
GGAAAGAGGG AAGCCCTTCG CACCGCGAAA GAGTATCGAG TGCGACATCC

ApaLI

2451 TATCTCAGTT CGGTGTAGGT CTTTCGCTCC AAGCTGGGCT GTGTGCACGA
ATAGAGTCAA GCCACATCCA CCAAGCGAGG TTCGACCCGA CACACGTGCT

22/63
FIG. 8. (CONTINUED)

2501 ACCCCCCGTT CAGCCCGACC GCTGCGCCTT ATCCGGTAAC TATCGTCTTG
TGGGGGGCAA GTCGGGCTGG CGACGCGGAA TAGGCCATTG ATAGCAGAAC
.....
2551 AGTCCAACCC GGTAAGACAC GACTTATCGC CACTGGCAGC AGCCACTGGT
TCAGGTTGGG CCATTCTGTG CTGAATAGCG GTGACCGTCG TCGGTGACCA
.....
2601 AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG AGTTCTTGAA
TTGTCCTAAT CGTCTCGCTC CATACTCCG CCACGATGTC TCAAGAACTT
.....
2651 GTGGTGGCCT AACTACGGCT ACACTAGAAG GACAGTATTT GGTATCTGCG
CACCACCGGA TTGATGCCGA TGTGATCTTC CTGTCATAAA CCATAGACGC
.....
2701 CTCTGCTGAA GCCAGTTACC TTCGGAAAAA GAGTTGGTAG CTCTTGATCC
GAGACGACTT CCGTCAATGG AAGCCTTTTT CTCAACCATC GAGAACTAGG
.....
2751 GGCAAACAAA CCACCGCTGG TAGCGGTGGT TTTTTGTTT GCAAGCAGCA
CCGTTTGTTC GGTGCGGACC ATCGCCACCA AAAAAACAAA CGTTCGTCGT
.....
2801 GATTACGCGC AGAAAAAAG GATCTCAAGA AGATCCTTTG ATCTTTTCTA
CTAATGCGCG TCTTTTTTTC CTAGAGTTCT TCTAGGAAAC TAGAAAAGAT
.....
2851 CGGGGTCTGA CGCTCAGTGG AACGAAACT CACGTTAAGG GATTTTGGTC
GCCCCAGACT GCGAGTCACC TTGCTTTTGA GTGCAATTC CTAAAACCAG
.....
2901 ATGAGATTAT CAAAAAGGAT CTTACCTAG ATCCTTTTAA ATTAAAAATG
TACTCTAATA GTTTTTCCTA GAAGTGGATC TAGGAAAATT TAATTTTAC
.....
2951 AAGTTTAAAT TCAATCTAAA GTATATATGA GTAAACTTGG TCTGACAGTT
TTCAAAATTT AGTTAGATT CATATATACT CATTGAACC AGACTGTCAA
.....
3001 ACCAATGCTT AATCAGTGAG GCACCTATCT CAGCGATCTG TCTATTTCTG
TGGTTACGAA TTAGTCACTC CGTGGATAGA GTCGCTAGAC AGATAAAGCA
.....
3051 TCATCCATAG TTGCCTGACT CCGCTCGTG TAGATAACTA CGATACGGGA
AGTAGGTATC AACGGACTGA GGGGCAGCAC ATCTATTGAT GCTATGCCCT
.....
3101 GGGCTTACCA TCTGGCCCCA GTGCTGCAAT GATACCGCGA GACCCACGCT
CCCGAATGGT AGACCGGGT CACGACGTTA CTATGGCGCT CTGGGTGCGA
.....
3151 CACCGGCTCC AGATTTATCA GCAATAAACC AGCCAGCCGG AAGGGCCGAG
GTGGCCGAGG TCTAAATAGT CGTTATTTGG TCGGTCGGCC TTCCCGGCTC
.....
3201 CGCAGAAGTG GTCCTGCAAC TTTATCCGCC TCCATCCAGT CTATTAATTG
GCGTCTTCAC CAGGACGTTG AAATAGGCGG AGGTAGGTCA GATAATTAAC
.....
3251 TTGCCGGGAA GCTAGAGTAA GTAGTTCGCC AGTTAATAGT TTGCGCAACG
AACGGCCCTT CGATCTCATC CATCAAGCGG TCAATTATCA AACGCGTTGC
.....
3301 TTGTTGCCAT TGCTACAGGC ATCGTGGTGT CACGCTCGTC GTTTGGTATG
AACAACGGTA ACGATGTCCG TAGCACCACA GTGCGAGCAG CAAACCATAC
.....
3351 GCTTCATTCA GCTCCGGTTC CCAACGATCA AGGCGAGTTA CATGATCCCC
CGAAGTAAGT CGAGGCCAAG GGTGCTAGT TCCGCTCAAT GTACTAGGGG
.....
3401 CATGTTGTGC AAAAAAGCGG TTAGCTCCTT CGTCCCTCCG ATCGTTGTCA
GTACAACACG TTTTTCGCC AATCGAGGAA GCCAGGAGGC TAGCAACAGT
.....
3451 GAAGTAAGTT GGCCGAGTG TTATCACTCA TGGTTATGGC AGCACTGCAT
CTTCATTCAA CCGGCGTCAC AATAGTGAGT ACCAATACCG TCGTGACGTA
.....

FIG. 8. (CONTINUED) 23/63

```

3501 AATTCTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTTCTG TGA CTGGTGA
    TTAAGAGAAT GACAGTACGG TAGGCATTCT ACGAAAAGAC ACTGACCACT
.....
3551 GTACTCAACC AAGTCATTCT GAGAATAGTG TATGCGGCGA CCGAGTTGCT
    CATGAGTTGG TTCAGTAAGA CTCTTATCAC ATACGCCGCT GGCTCAACGA
.....
3601 CTTGCCCGGC GTCAATACGG GATAATACCG CGCCACATAG CAGAACTTTA
    GAACGGGCGG CAGTTATGCC CTATTATGGC GCGGTGTATC GTCTTGAAAT
.....
3651 AAAGTGCTCA TCATTGAAA ACGTTCTTCG GGGCGAAAAC TCTCAAGGAT
    TTTCACGAGT AGTAACCTTT TGCAAGAAGC CCCGCTTTTG AGAGTTCCTA
.....
                                     ApaLI
                                     -----
3701 CTTACCGCTG TTGAGATCCA GTTCGATGTA ACCCACTCGT GCACCCAAT
    GAATGGCGAC AACTCTAGGT CAAGCTACAT TGGGTGAGCA CGTGGGTGA
.....
3751 GATCTTCAGC ATCTTTTACT TTCACCAGCG TTTCTGGGTG AGCAAAAACA
    CTAGAAGTCG TAGAAAATGA AAGTGGTCCG AAAGACCCAC TCGTTTTTGT
.....
3801 GGAAGGCAAA ATGCCGCAA AAAGGGAATA AGGGCGACAC GGAAATGTTG
    CCTCCGTTT TACGGCGTTT TTTCCCTTAT TCCCGCTGTG CCTTTACAAC
.....
3851 AATACTCATA CTCTTCCTTT TTCAATATTA TTGAAGCATT TATCAGGGTT
    TTATGAGTAT GAGAAGGAAA AAGTTATAAT AACTTCGTAA ATAGTCCCAA
.....
3901 ATTGTCTCAT GAGCGGATAC ATATTTGAAT GTATTTAGAA AAATAAACAA
    TAACAGAGTA CTCGCCTATG TATAAACTTA CATAAATCTT TTTATTGTT
.....
3951 ATAGGGGTTT CGCGCACATT TCCCCGAAAA GTGCCACCTG ACGTCTAAGA
    TATCCCCAAG GCGCGTGTA AGGGGCTTTT CACGGTGAC TGCAGATTCT
.....
4001 AACCATTATT ATCATGACAT TAACCTATAA AAATAGGCGT ATCAGAGGC
    TTGGTAATAA TAGTACTGTA ATTGGATATT TTTATCCGCA TAGTGCTCCG
.....
4051 CCTTTCGTCT CGCGCGTTTC GGTGATGACG GTGAAAACCT CTGACACATG
    GGAAAGCAGA GCGCGCAAAG CCACTACTGC CACTTTTGA GACTGTGTAC
.....
4101 CAGCTCCCGG AGACGGTCAC AGCTTGTCTG TAAGCGGATG CCGGGAGCAG
    GTCGAGGGCC TCTGCCAGTG TCGAACAGAC ATTGCGCTAC GGCCCTCGTC
.....
4151 ACAAGCCCGT CAGGGCGCGT CAGCGGGTGT TGGCGGGTGT CGGGGCTGGC
    TGTTCCGGCA GTCCCCGCA GTCGCCACA ACCGCCACA GCCCCGACCG
.....
                                     ApaLI
                                     -----
4201 TTAACATGCG GGCATCAGAG CAGATTGTAC TGAGAGTGCA CCATATCGAC
    AATTGATACG CCGTAGTCTC GTCTAACATG ACTCTCACGT GGTATAGCTG
.....
4251 GCTCTCCCTT ATGCGACTCC TGCATTAGGA AGCAGCCCAG TAGTAGGTTG
    CGAGAGGGAA TACGCTGAGG ACGTAATCCT TCGTCGGGTC ATCATCCAAC
.....
4301 AGGCCGTTGA GCACCGCCGC CCAAGGAAT GGTGCATGCA AGGAGATGGC
    TCCGGCAACT CGTGGCGGCG CGGTTCTTA CCACGTACGT TCCTCTACCG
.....
4351 GCCCAACAGT CCCCCGGCCA CGGGGCTGTC CACCATACCC ACGCCGAAAC
    CGGGTTGTCA GGGGGCCGGT GCGCCGACG GTGGTATGGG TCGCGCTTTG
.....
4401 AAGCACTAAT AGGAATTGAT TTGGATGGTA TAAACGAAA CAAAAAAG
    TTCGTGATTA TCCTTAACTA AACCTACCAT ATTTGCCTTT GTTTTTTTT
.....

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24/63

FIG. 8. (CONTINUED)

4451 AGCTGGTACT ACTTTCCTTA AAATTATTTT ATTATTTGAT TTTATTTAAT
TCGACCATGA TGAAAGAAAT TTTAATAAAA TAATAAACTA AAATAAAATTA
.....

4501 AGTATATATT ATATTTTGAA CGTAGATTAT TTTGTTGAAA GTTGCTGTAG
TCATATATAA TATAAACTT GCATCTAATA AAACAACCTT CAACGACATC
.....

4551 TGCCATTGAT TCGTAACACT AATCTGTAT TAGTCATTCC TCTTGTTGA
ACGGTAACTA AGCATTGTGA TTAAGACATA ATCAGTAAGG AGAACAACT
.....

4601 TAGTATCCAA AAAAACGGCT ATTTTTTGC AATCTTATTT CCTGCATATT
ATCATAGGTT TTTTGCCGA TAAAAAACG TTAGAATAAA GGACGTATAA
.....

4651 ATACAGATAA CATAATGAAA GAAAAATCT TTTTTTTGT TCTTCAATGA
TATGTCTATT GTATTACTTT CTTTTTTAGA AAAAAAACA AGAAGTTACT
.....

4701 TGATTTCAAC CATTCTTTTA AACATTGATC AATTCCTGAG CAACAACCCC
ACTAAAGTTG GTAAGAAAAT TTGTAAGTAG TTAAGGACTC GTTGTGGGG
.....

4751 ATACACACTG GTTTATATAC CGCCCCCTTT ACAGTTGAAG AAAGAAATAG
TATGTGTGAC CAAATATATG GCGGGGAAAA TGTCAACTTC TTTCTTTATC
.....

4801 AAATAGAAAT AGCAACAAA AGATATGACA GTCAACACTA AGACCTATAG
TTATCTTTA TCGTTTGTG TCTATACTGT CAGTTGTGAT TCTGGATATC
.....

4851 TGAGAGAGCA GAAACTCATG CCTCACCAGT AGCACAGCGA TTATTTGAT
ACTCTCTCGT CTTTGAGTAC GGAGTGGTCA TCGTGTGCT AATAAGCTA
.....

4901 TAATGGAAC GAAGAAAACC AATTTATGTG CATCAATTGA CGTTGATACC
ATTACCTTGA CTTCTTTTGG TAAATACAC GTAGTTAACT GCAACTATGG
.....

AvaI

4951 ACTAAGGAGT TCCTCGAGTT AATTGATAAA TTAGGTCCTT ATGTATGCTT
TGATTCCTCA AGGAGCTCAA TTAATATTTT AATCCAGGAA TACATACGAA
.....

5001 AATCAAGACT CATATTGATA TAATCAATGA TTTTCCTAT GAATCCACTA
TTAGTTCTGA GTATAACTAT ATTAGTTACT AAAAAGGATA CTTAGGTGAT
.....

5051 TTGAACCATT ATTAGAACTT TCACGTAAAC ATCAATTTAT GATTTTGA
AACTTGGTAA TAATCTTGAA AGTGCATTG TAGTTAAATA CTAAAACTT
.....

5101 GATAGAAAAT TTGCTGATAT TGGTAATACC GTAAAGAAAC AATATATTGG
CTATCTTTTA AACGACTATA ACCATTATGG CATTCTTTG TTATATAACC
.....

5151 TGGAGTTTAT AAAATTAGTA GTTGGGCAGA TATTACCAAT GCTCATGGT
ACCTCAAATA TTTAATCAT CAACCCGTCT ATAATGGTTA CGAGTACCAC
.....

5201 TCACTGGGAA TGGAGTGGT SAAGGATTAA AACAGGGAGC TAAAGAAACC
AGTGACCTT ACCTACCAAT CTCCTAATT TTGTCCCTCG ATTTCTTTGG
.....

5251 ACCACCAACC AAGAGCCAAG AAGCTTATTG ATGTTAGCTG AATTATCATC
TGGTGGTTGG TTCTCGGTTT TCCCAATAAC TACAATCGAC TTAATAGTAG
.....

5301 AGTGGGATCA TTAGCATATG SAGAATATTC TCAAAAAACT GTTGAAATTG
TCACCCTAGT AATCGTATAC CTCTTATAAG AGTTTTTTGA CAACTTTAAC
.....

5351 CTAAATCCGA TAAGGAATTT TTATTGGAT TTATTGCCCA ACGTGATATG
GATTTAGGCT ATTCCTTAAA CAATAACCTA AATAACGGGT TGCATATAC
.....

FIG. 8. (CONTINUED) 25/63

5401 GGTGGCCAAG AAGAAGGATT TGATTGGCTT ATTATGACAC CTGGAGTTGG
CCACCGGTTT TTCTTCTTAA ACTAACCAGAA TAATACTGTG GACCTCAACC
.....
5451 ATTAGATGAT AAAGGTGATG GATTAGGACA ACAATATAGA ACTGTTGATG
TAATCTACTA TTCCACTAC CTAATCCTGT TGTATATCT TGACAACTAC
.....
5501 AAGTTGTTAG CACTGGAACAT GATATTATCA TTGTTGGTAG AGGATTGTTT
TTCAACAATC GTGACCTTGA CTATAATAGT AACCAACCATC TCCTAACAAA
.....
5551 GGTAAAGGAA GAGATCCAGA TATTGAAGGT AAAAGGTATA GAAATGCTGG
CCATTTCCTT CTCTAGGTCT ATAACCTCCA TTTTCCATAT CTTTACGACC
.....
5601 TTGGAATGCT TATTTGAAAA AGACTGGCCA ATTATAAATG TGAAGGGGGA
AACCTTACGA ATAACTTTT TCTGACCGGT TAATATTAC ACTTCCCCCT
.....
5651 GATTTTCACT TTATTAGATT TGTATATATG TAGAATAAAT AAATAAATAA
CTAAAAGTGA AATAATCTAA ACATATATAC ATCTTATTTA TTTATTTATT
.....
5701 GTTAAATAAA TAATTAAATA AGGGTGGTAA TTATTACTAT TTACAATCAA
CAATTTATTT ATTAATTTAT TCCACCATT AATAATGATA AATGTTAGTT
.....
5751 AGGTGGTCCT TCTAGCTGTA ATCCGGGCG AGCAACGGAA CATTTCATCAG
TCCACCAGGA AGATCGACAT TAGGCCCGTC GCGTTGCCTT GTAAGTAGTC
.....
5801 TGTAATAATG GAATCAATAA AGCCCTGCGC TCATGAGCCC GAAGTGGCGA
ACATTTTAC CTTAGTTATT TCGGACGCG AGTACTCGGG CTTACCCGCT
.....
5851 GCCCATCTT CCCCATCGGT GATGTCGGCG ATATAGGCGC CAGCAACCGC
CGGGCTAGAA GGGGTAGCCA CTACAGCCGC TATATCCGCG GTCGTTGGCG
.....
5901 ACCTGTGGCG CCGCAGCGCG CAGGGTCAGC CTGAATACGC GTTTAATGAC
TGGACACCGC GCGTCGCGC GTCCAGTCG GACTTATGCG CAAATTACTG
.....
5951 CAGCACAGTC GTGATGGCAA GGTCAGAATA GCCCAAGTCG GCCGAGGGGC
GTCGTGTCAG CACTACCGTT CCAGTCTTAT CGGGTTCAGC CGGCTCCCCG
.....
6001 CTGTACAGTG AGGGAAGATC TGATATTGAC GAAGAGGAAC CAATGTAACG
GACATGTCAC TCCCTTCTAG ACTATAACTG CTTCTCCTTG GTTACATTGC
.....
6051 TTACACTGAA GAAAACACAC AATAAACGGG AAGAAACGGT GTAAAAGTGT
AATGTGACTT CTTTGTGTG TTATTTGCC TTCTTGCCA CATTTTCA
.....
6101 GAAAATAATT TTTGAATATC ATTTCCCTTG GTTTAATTCC AACGAAACG
CTTTTATTAA AAACCTATAG TAAAGGGAAC CAAATTAAGG TTGCTTTGC
.....

EcoRI

6151 TGTTTTTTTT AGAGAATGGG AATCTTATT GGATGTCTAG ATTGTTTGT
ACAAAAAAA TCTCTTACCC TTAAGAATAA CCTACAGATC TAACAAACAA
.....

ApaLI

6201 TACTCCAGAC TGTGCACAAA AACGTTTGA TGGATGATCA GAAGATATTT
ATGAGGTCTG ACACGTGTTT TTGCAACCT ACCTACTAGT CTTCTATAAA
.....
6251 TTAGGCTTAG CTCTAAATAT AAGAAATGAT GCTTGAAAAA CCAGACAGAA
AATCCGAATC GAGATTTATA TCTTTACTA CGAACTTTTT GGTCTGTCTT
.....
6301 ATTGAGTTT AAAAATTGGT AATGTGAGGT ATTAGTCAAC TAACCAATA
TAACCTCAAAG TTTTAACCA TCACTCCA TAATCAGTTG ATTGGTTTAT
.....

26/63

FIG. 8. (CONTINUED)

6351 ACAATGCAAA CCGGTTGATA CATTTCATT TGAAAATAAT GAACTGGAA
TGTTACGTTT GGCCAACAT GTAAAGTAAA ACTTTTATTA CTTTGACCTT

6401 TTGGATGACC AGCACACAAA CACATAAAGT AATTATGGGA ATTAGAAGCG
AACCTACTGG TCGTGTGTTT GTGTATTTC TTAATACCCT TAATCTTCGC

6451 AACATAGAGG AGTACTTGGC CACGAACAGA ATACAAGTGG GAACACTATT
TTGTATCTCC TCATGAACCG GTGCTTGTCT TATGTTCCACC CTGTGATAA

6501 TTCTCCATTG TTTTAGTTCT GTTTTTTTGT CAGCCTAGTT TTGTGCTATG
AAGAGGTAAC AAAATCAAGA CAAAAAACA GTCGGATCAA AACACGATC

HindIII

6551 TGTAAGAAAT ATTGCCAAGA AAAAAAGCTT GTTTTGTGGC CAGTGTCCGA
ACATTTTMTA TAACGGTTCT TTTTTCGAA CAAACACCG GTCACAGGCT

6601 AAAAAATTTT GGGGAATCTT CGGATTAATT TATGTTTCA
TTTTTTAAAA CCCCTTAGAA GCCTAATTAA ATACAAAAGT

27/63

FIG. 9.

ATGTATGTTTATAAGAGAGATGGCCGTAAAGAGCCAGTACGTTTCGACAAAAT
CACTGCCAGAGTTCAAAGATTATGTTA
CGGTTTGAATCCAAACCACGTTGAACCAGTTGCTATTACCCAAAAAGTTATATC
AGGTGTTTACCAGGGGGTTACTACTA
TTGAGTTGGACAACCTTGGCTGCAGAAATTGCTGCTACAATGACAACAATTAC
CCAGATTACGCTGTCTTAGCCGCTAGA
ATTGCCGTATCAAATTTACATAAGCAAACCACCAAACAGTATTCCAAAGTGTC
TAAGGATTTATATGAATACATTAATCC
TAAGACTGGGTACACTCTCCTATGATTTCCAAGGAAACCTACGACATCATTAT
GGAACACGAAGATGAATTAACCTCAG
CCATTGTTTACGACAGAGATTTTAACTACAATTATTTTGGGTTCAAGACTTTGG
AAAGATCATATTTGTTACGTATCAAC
GGTAAGGTTGCTGAAAGACCACAACATTTGATCATGAGGGTTGCTGTCGGTAT
TCACGGTAATGATATACCAAGGGTCAT
TGAAACCTATAACTTGATGTCTCAAAGATTCTTCACCCATGGTTCTCCTTGTTTA
TTTAACGCTGGTACACCAAGACCAC
AAATGTCCTCATGTTTCTTGCTTGCTATGAAGGATGATTCTATTGAAGGTATTT
ACGACACTTTGAAATCGTGTGCTTTG
ATCTCAAAAAGTGCTGGAGGAATCGGTTTACACATCCACAACATTCGTTCTACC
GGTGCTTACATTGCTGGTACCAATGG
TACTTCTAATGGTATTATTCCAATGGTAAGAGTATTCAATAACACTGCACGTTA
TGTCGACCAAGGTGGTAACAAGAGAC
CTGGTGCCTTTGCCTTGTACTTAGAACCATGGCACAGTGACATTTTTGATTTC
TTGATATTAGAAAGAATCACGGTAAA
GAAGAAATCAGAGCCAGAGATTTGTTCCCAGCTTTGTGGATTCCAGATTTGTTC
ATGAAAAGAGTTGAACAAAATGGTGA
CTGGACTTTATTCTCACCAAATGAGGCCCCAGGCTTGGCTGATGTTTATGGTGA
CGAATTCGAAGAATTATACACCAAAT
ACGAAAAAGAAAACCGTGGTAGACAGACCATCAAAGCTCAAAAATTGTGGTA
TGCTATTTTGGGAGCCCAAACCTGAAACA
GGTACCCCATTTATGTTATATAAAGATTTCATGTAACAACAAATCCAACCAAAA
GAACTTGGGTATTATCAAATCTTCAA
CTTGTGTTGTGAAATTGTTGAATATTCTGCTCCAGATGAAGTTGCTGTTTGTA
CTTGGCTTCCATTGCCTTGCCATCAT
TTGTTGAAAATGATGAAAAAGTACTTGGTACAACCTTTGACAAATTACATCAG
GTCACTAAGGTTGTCACCCGTAACCTG
AACAGAGTTATTGACCGTAACCATTACCCAGTCCCAGAAGCTGAAAGATCAAA
CATGAGACACAGACCAATTGCTTTGGG
TGTTCAAGGTTTGGCTGATGCCTTTATGGAATTGAGATTACCATTTGACTCTCA
AGAAGCTAGAGAATTGAACATTCAAA

28/63

FIG. 9. (CONTINUED)

TTTTTGAGACTATCTACCATGCTGCTGTTGAAGCTTCAATTGAATTGGCTAAAG
AAGAAGGTGCCTACGAAACCTATCCA
GGTTCTCCAGCCTCTCAAGGTTTATTACAATTTGATTTGTGGAACAGAAAACCA
ACTGAATTATGGGATTGGGATACATT
AAAACAAGATTTGGCCAACATGGTATGAGAACTCCTTGTTGGTTGCACCAA
TGCCTACTGCTTCCACATCACAATTT
TGGGTAACAATGAATGTTTTGAACCATACTTCTAACATTTACTCTAGAAGAG
TATTAGCTGGAGAATTCCAATTGTC
AATCCATATTTATTGAAGGACTTGGTTGATTTGGGTGTCTGGAACGACGCTATG
AAAAGTAGTATTATTGCTAACAATGG
TTCTATCCAAGCCTTACCAACATCCCTGATGAAATCAAGGCATTGTACAAAA
CTGTCTGGGAAATCTCACAAAAACATA
TTATCGACATGGCTGCTGATAGAGCAGCATTTATTGATCAATCTCAATCATTAA
ACATTCACATCAAAGATCCAACAATG
GGTAAATTAACCAGTATGCACTTCTACGGTTGGAAGAAAGGTTTAAAGACTGG
TATGTACTACTTAAGAACACAAGCTGC
CAGTGCTGCTATTCAATTTACCATTGATCAAAAAGATTGCTGAGACTGCCGGTCA
TACGGTTGCAAACCTTGGACAAATTAA
ACATTAAGAAATATGTAAACAAAGGAAGAGTTGAGAGTGAGAATACCAGTGAT
GCTCCATACAAGTCACCATCAACCGAA
CCAACCTCATTAGAAAGTTCAGTTGCTGATTTGAAAATAAAAGATGAAGGTGA
AAAGCCAGCTGAAGACAAAACCATTTGA
AGAACTCGAAAATGACATTTATAGTGCCAAAGTTATCGCATGTGCTATTGATA
ATCCAGAATCTTGTACAATGTGTTCTG
GT

29/63

FIG. 10.

ATAGAACTGTTTGATATACAACTATCTCACTCCCAATTGTGACTTGAATAAATAATACCTATCACCTAGTAATCTTT
 ATCTTAACGTAACTCTGCAAGCAATCAATGTATAAAGCATAAAGATAAATCTTGGTGAGGTTTAAAGTTCAATAAT
 TATAATGAACAACTTAAAGGATGGTATCAACAAATTAAGGCTAGGTAGAACCATAGTGCTGTTCCGGAGTT
 CCGGTAGTTTGGGAAGTTGGGAAGTTGGATAGTTTGAGAAAGGTTCCGTGCTGATTCTAAATTAACAGAGAACGATAT
 AATGTACAAAAACATTTCAGAAATTTAAACAACTTTATATATATATTAATTCCTCTTGTGCATCAACTTCCCATTCG
 TGTGATGATGCTTTCCTGTTAAATATACCTTTAAGAACAGATTCACTATCTCAACTAATAATTAACCCCTTATACITTTT
 GTTTTGACATTCCATATGACACAAAGATCTGAAATAATTTTACCTCAAGGGATCTACTCATTCCTATCTCAAAACA
 CACATTCTTTGTATCACCATACTTTTGTAAACAGAGGAAACAAATAATTGACACCGCATGTCAATTAACCTATAGCACTA
 TCACACAAATCAAGGATTTACAAATAGTGGAAATGTCAAAATCATGTATATTAATTAACACATTACACATATTTATTTCA
 GGTACATAAATCTCAATATCTAAACCTTCAAAATGGTACTGTACCTTAACCTTTCCTTCATGTCTAGTTGAATATTTAT
 ACTTGCTAATGTCAAAATCAATGCTTCACACATTCCAGTTGT

30/63

FIG. 11.

GCAAGATCTAACTCCAGTTTTTGGTGTAAATGTTACACAAGCAACAATAATATATCGAAGAAAGCCCCCAATATTCT
 CTTCTACAAATTACGAATAATGTTTCACA:GTATGAAGAGCTTTATCTATACTATTTCTCCTCCAACTCTAGCAGTGAG
 AATGATACTGATATCTCCTAT:AGGATACAGTTATCTATTATAGTATATAATATCATGGAGATAAATATATTAA
 TCGATGGAGTTAACGAGAAACAATACACCCCAATTTGCGAGCAAAATGAGACAATTCACAGAAATAAACAAGAAAG
 ACAATTACTCCATTCAATAATTCACAA:AAATAATAACAAGAACAAAGTACTAACAAATAACATCCTAATTTCA
 CTTTGAATACTTTACATCTCACTTCTAAGATTAAATAAAGCGATGCATATTCATCAGAAATTTAGTGTATACAATA
 TGCAGGTGATTTATGAGCCAGGTGAACAA:TCCTTACTAATAATCTAGGAGTTGTTTATATACAGTATTTTGTCTAAC
 CTGTCTTAAGGTATACAGATAGATTGTAATCGGTTAGAAATACAAGAAAGGTGGTTGTGGACTTGGTGGTGG
 CAAATTTGAATGATATATTGTTATCTCAAGTATAGCAATACAGGCAAGGCTGCAACAACAAGAACTTGGATT
 GTCGCAATCTCTTCACCCCTT:CAGAAATG:CCTCGTGTATGTGATCAAT

31/63

FIG. 12.

CCCCGTTAACCACCTTCTAGGGTATACCATTTTCATCTGACTGAATAACTGGTTAG
TCGATTTGTTGTTGAAGAAAAGTGAC
CACCTAGTTTTTTCTGCCAACATTTTTTGCGATGAGCCGTCGACGCGTTGTCTTT
TTCTACCCACGTTTAACAATCTTG
CCAGTCAATTCCCTAGCCAAATAAACTTTAGACTCACAACTCTAACACTGACTC
GTGCCCCCCTGTTTAAACTCTAAATT
ACTTCACAGAGCCTTTACTACCTTAAATTTARGRTTWTSKAKKGTTTCTGTTTTT
TTGCAAATCACCCCTGACTYGTTTTT
TTTTCAGCCAGGTTTTTCGTTAAAATCTGACCAAAAAATTTACRACTCCTATWT
TTAAAACCTCYAAAWWACAATTAAAC
TCAATTCAGACAAGTCCTTCTGCTCATTCTGAGTCTTCTCTATTGTCTTTTGACT
TTTTGTGTGTGACTATTTTCATGAT
CACCCCGTTTCTTGCATTTTTTTCAGTCAACTTTTTCTCAAAATCAAGCCAAAAA
AACACACCTTTAACTACCTATACAA
CGCAAACCTATTCAAAACA

32/63

FIG. 13.

ATGACTACTTCCAAGGAACTTTCTTTTCACTTCAGAATCCGTTGGTGAAGGT
CACCCAGATAAGATTTGTGACCAAGT
CTCCGATGCCATTTTAGATGCTTGTTTAGCTGTTGATCCATTGTCAAAAGTTGCT
TGTGAAACTGCTGCCAAAACCGGTA
TGATTATGGTTTTTGGTGAAATTACCACTAAAGCTCAATTGGATTATCAAAAAA
TCATTAGAGACACCATTAAACACATT
GGTTACGACGATTCTGAAAAAGGTTTTGATTACAAGACTTGTAACGTCTTGGTT
GCAATTGAACAACAATCTCCAGATAT
TGCTCAAGGTTTACATTACGAAAAAGCTTTGGAAGAGTTGGGTGCTGGTGATC
AAGGTATTATGTTTGGTTATGCCACCG
ATGAAACCGATGAAAAATTGCCATTGACCATTTTATTGGCCCACAAATTGAAT
GCTGCCTTGGCTTCTGCCAGAAGATCA
GGTTCCTTGCCATGGTTGAGACCAGATACCAAAACCCAAGTCACCATCGAGTA
TGAAAAAGATGGTGGTGCA GTTATCCC
AAAAAGAGTCGACACAATTGTTATTTCCACTCAACATGCCGAAGAAATCACCA
CCGAAAATTTGAGAAAAGAAATTATTG
AACATATCATCAAGCAAGTCATCCCAGAACATTTATTAGACGACAAAACCTATC
TACCACATTCAGCCATCAGGCAGATTC
GTCATTGGTGGTCCCCAAGGTGATGCTGGTTTGACTGGTAGAAAGATCATTGTT
GACACCTATGGTGGTTGGGGTGCA
TGGTGGTGGTGCCTTCTCAGGCAAGGATTTCTCCAAAGTTGATAGGTCTGCTGC
TTATGCCGCTCGGTGGGTTGCTAAGT
CGTTGGTGACCGCCGGATTGGCCAAAAGGGCCTTGGTGCAGTTCTCCTATGCTA
TTGGGGTTGCTGAACCCACCAGCATT
TATATAGACACCTATGGGACATCTAAATTGAGCACCGAAGCCCTTGTAAGAAAT
TATCAAGAATAATTTTGACTTACGCCC
TGGCGTAATTGTAAAAGATTAGATTTGGCTCGTCCTATTTATTTTAAAACCGC
TTCTTACGGACATTTTACTAACCAAG
AAAATTCTTGGGAACAACCAAAAAAATTAAAATTT

33/63

FIG. 14.

1 MYVYKPDGRX EPVRFDKITA RVQRLOYGLN P:HVPEVAIT QKVISGVYQG
 31 VTTIELDNLA AEIAATMTTI HPDYAVLAAR IAVENLNKQT TKQYSKVSKE
 101 LYEYINPKTC LHSFMISKET YDILMEHEDE LNSAIVYDRD FTYNYFGFKT
 151 LERSYLLRIN GTVAERPQEL IMPVAVGIGH NDIPRVIETY NLMSQRFFTH
 201 GSPCLFNAGT FRPMSSCFL LAMKDDSTEG IYDTLKSCAL ISKSAGGIGL
 251 HINIRSTGA YIASTNGTSH GIIPMURVEN NTARYVDQGG NKRPGAFALY
 301 LEFWHSDFED FIDIRKNHGK EETARADLFP ALWIPDLFMK RVEZQNGEWL
 351 FSPNEAPCLA DVGDEFEEL YTRYEKENRG RQTIKAQKLW YAILGAYTET
 401 GTFFMLYKDS CHXASNQKNL GIIKSSNLCC EIVEYSAPDE VAVCNLASIA
 451 LPSFVENDEK STWAFEXKH QVTKVWTRNL NRVIDRNHYF VPEAERSMYR
 501 HRPIALGVQG LACAFMEIRL PFDSQEARBL NIQCFETIYH AAVEASTELA
 551 KEEGAYETYP GSPASGGLLQ FDLWNRKETE LWDWDTLKQD LAXHGMNSEL
 601 LVAPMPTAST SIIIGNNECF SPYTSNIYSE RVLAGEFQIV NPYLLZDLVD
 651 LGVANDAMES SIIANGSIQ ALPNIPDEIK ALYKTVWEIS QKHIIDMAAD
 701 RAAFIDQSQS LNNIXDPTX GKLTSMHYG WKXGLKTGMY YLRTQAASAA
 751 IQFTIDQKIA ETASHTVAIL DKLNIKHYVN KGRVESENTS DAPYKSFSTE
 801 PTSLESSVAD LKXDEGEKF AEDKTIEELE NDIYSAXVIA CAIENPESCT
 851 MCSC

*34/63**FIG. 15.*

1 MITSKETFLF TSZSVGZGKF DKICDQVSDA ILDACLAUDF LSKVACETAA
51 KTGMIN/EGE ITTKAQLDYQ KIIFDTIKHI GYDESEKGFY YKTCNVLVAI
101 EQQSPDIAGG IHYKALBEL GAGDQGIMFG YATDETDEKL PATILLAKKL
151 NAALASARNS GSLPWLRPOT KTQVTIEYEK DGGAVIPKRV DTIVISTQHA
201 EEITTENLKK ETEHIIKQV IPEHLLDOKT IYHIQPSGRF VIGGPGGDAG
251 LTGRKIIVTT YGGWJAHGOG AFSGKDFSKV DRSAAYAARN VAKSLVTAGL
301 AKRALVQFSY AGWAEPSTI YIDTYGTSKL STEALVEIHK NNFDLRPGVI
351 VYZDLARPI YKXASVGHF TNQENSWEQF KKLKF

35/63

FIG. 16.

RH170498 AF101-AF150 (16 hours)
glucose/maltose vs galactose/maltose
AF110

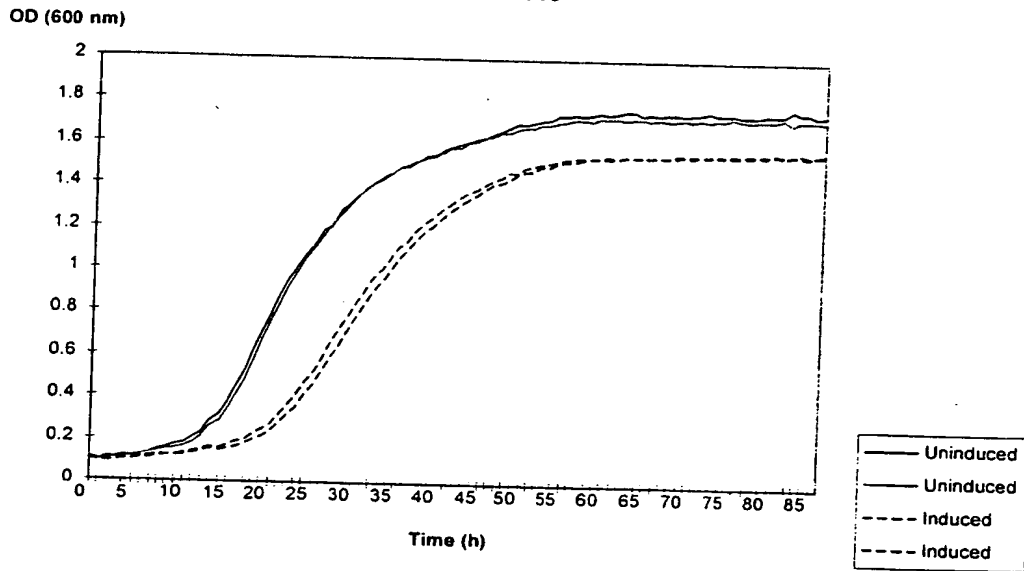
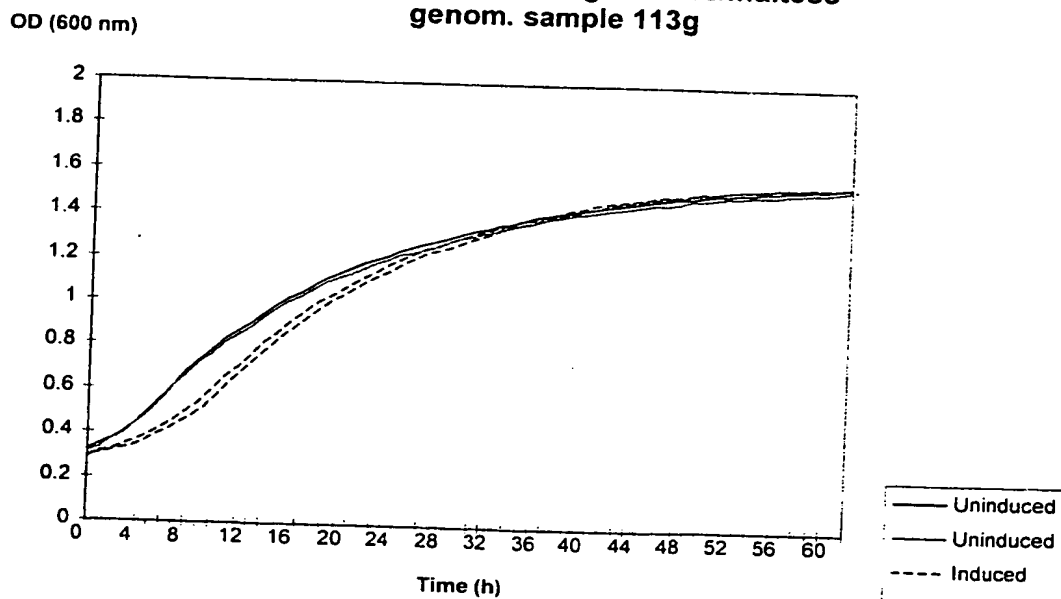


FIG. 17.

C. albicans library screening experiment 28/11/97
glucose/maltose vs galactose/maltose
genom. sample 113g



36/63

FIG. 18.

RH170498 AF101-AF150 (16 hours induction).
glucose/maltose vs galactose/maltose
AF117

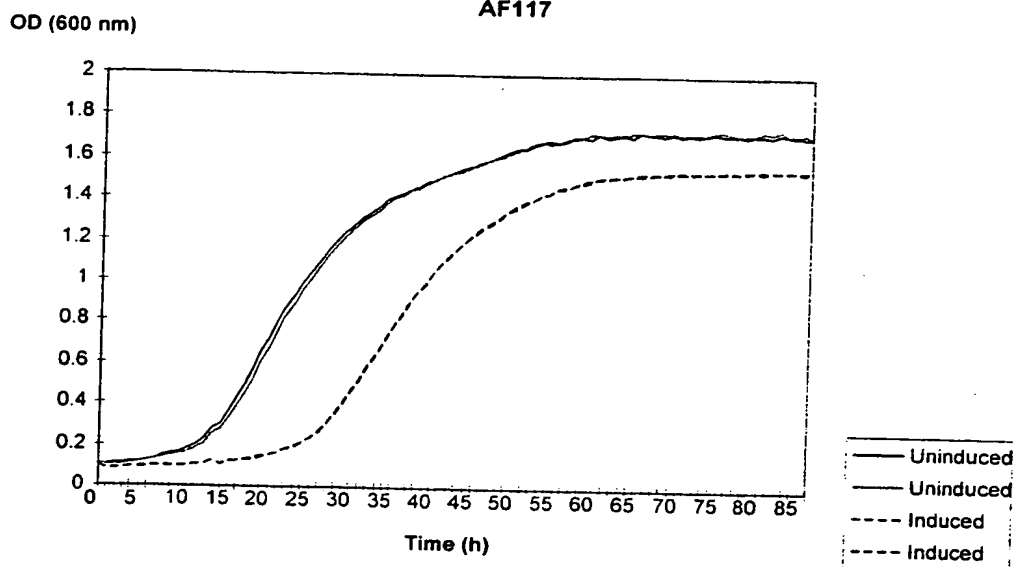
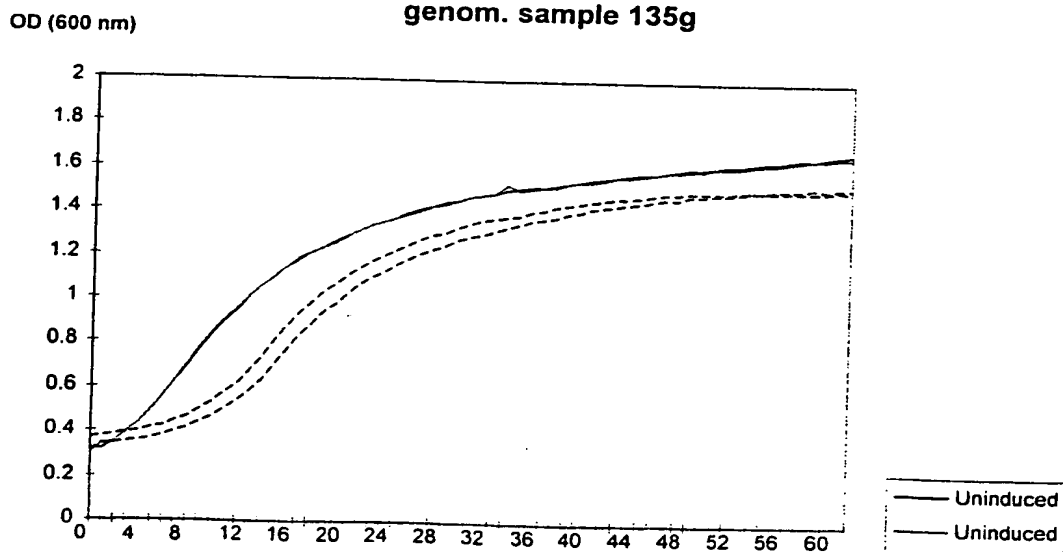


FIG. 19.

C. albicans library screening experiment 28/11/97
glucose/maltose vs galactose/maltose
genom. sample 135g



37/63

FIG. 20.

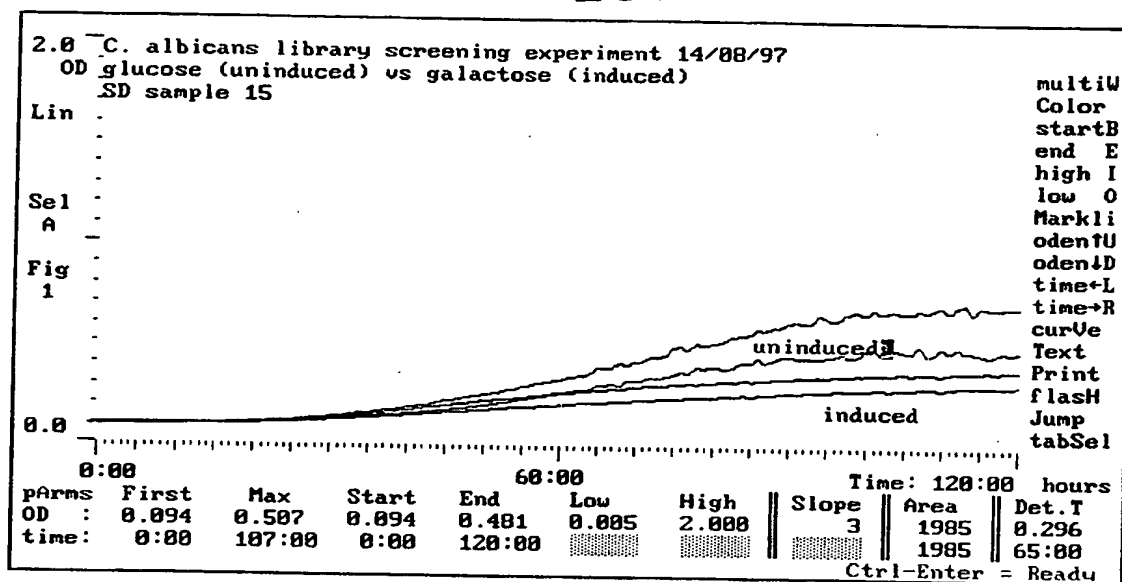
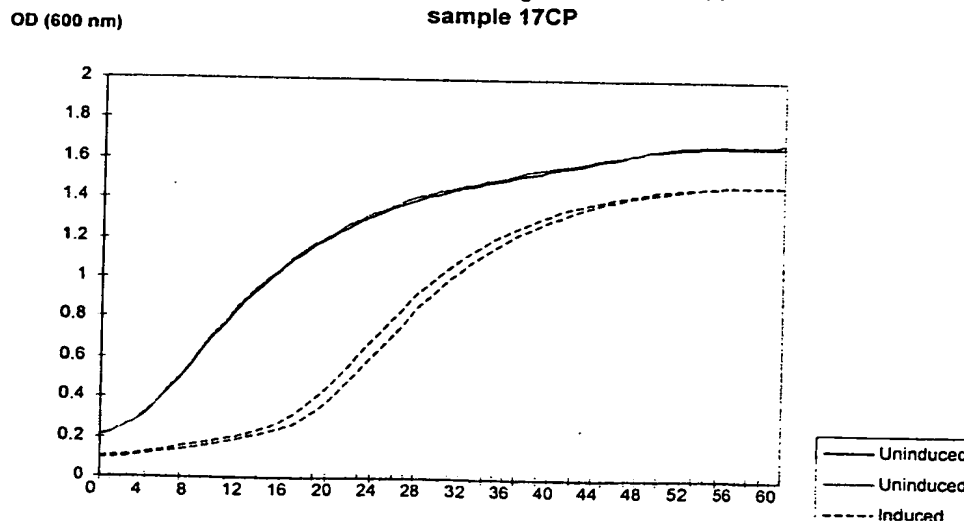


FIG. 21.

C. albicans library screening experiment 31/03/98
 glucose/maltose vs galactose/maltose
 sample 17CP



38/63

FIG. 22.

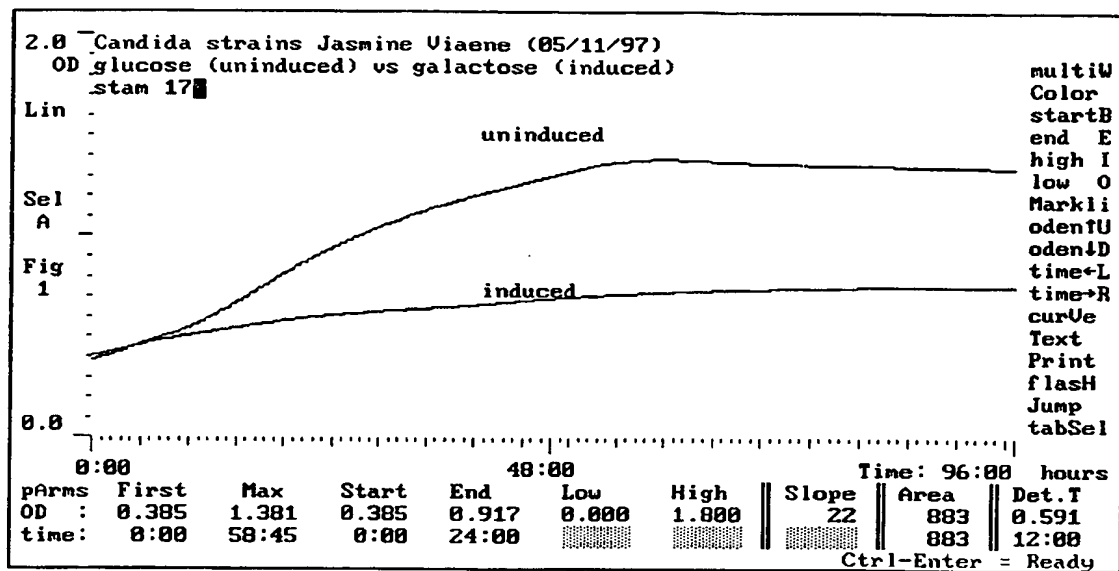
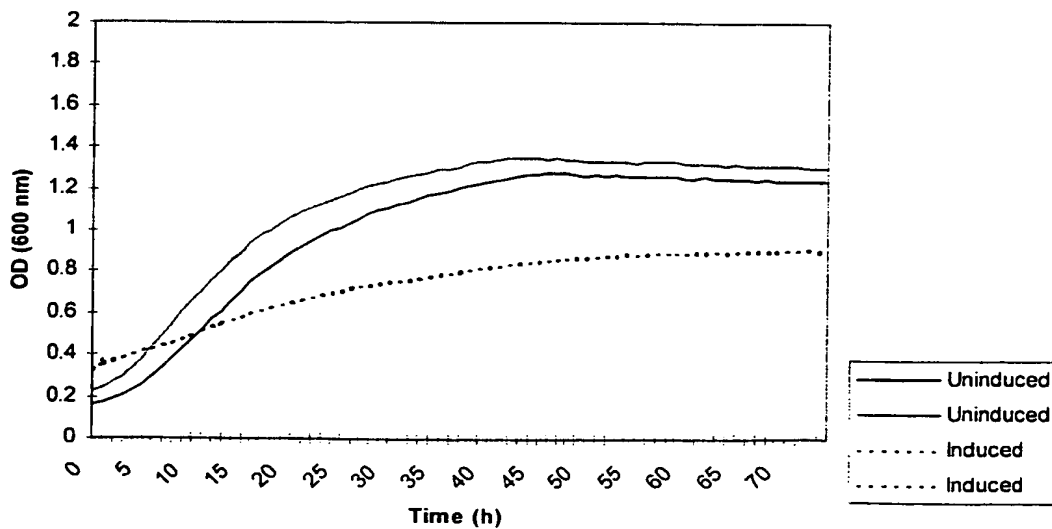


FIG. 23.

C. albicans library screening experiment 15/12/97
glucose vs galactose
genom. sample 190g



39/63

FIG. 24.

C. albicans library screening experiment 15/12/97
glucose vs galactose
genom. sample 207g

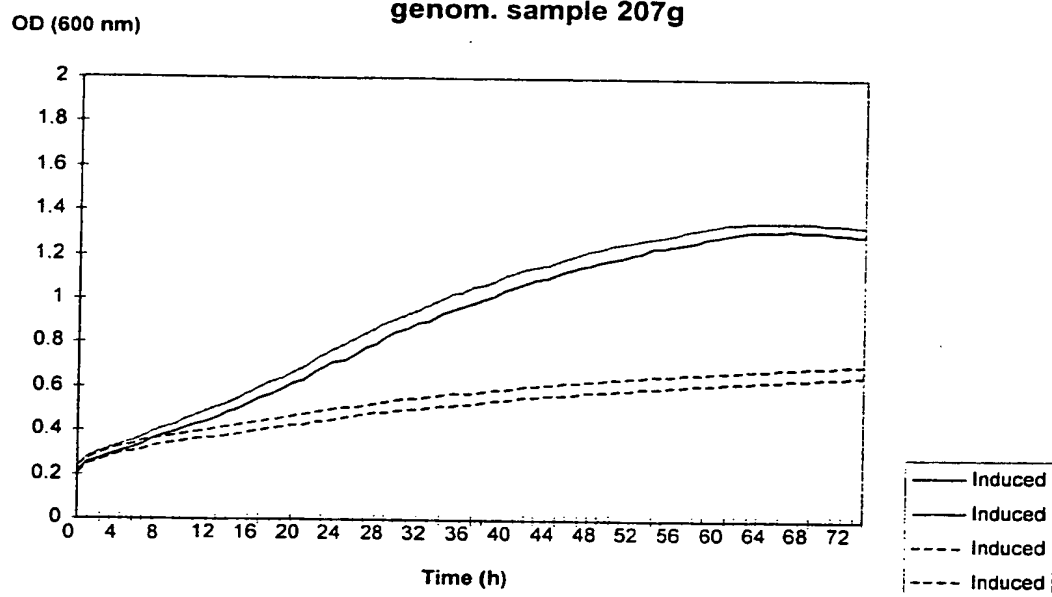
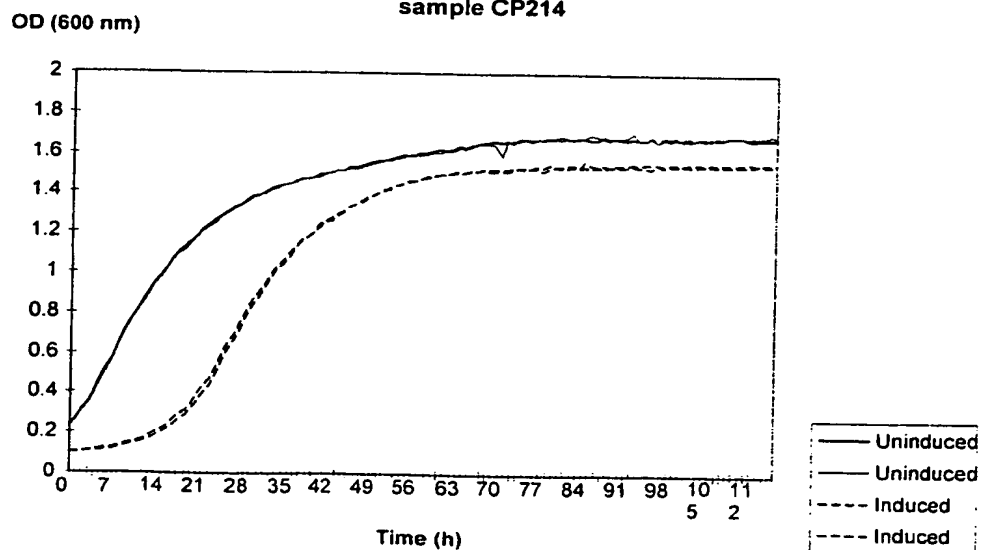


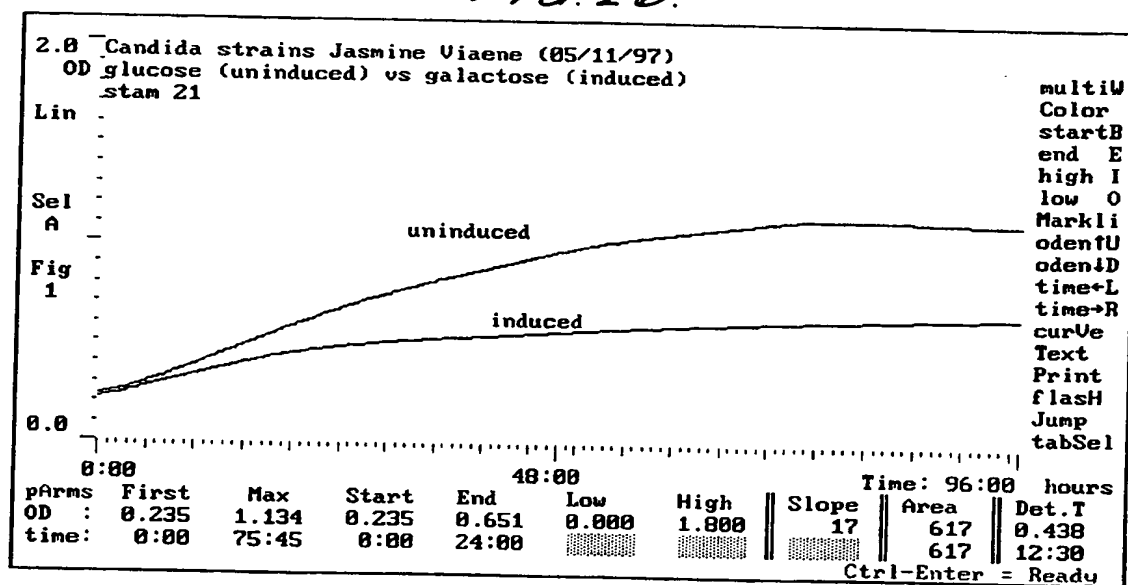
FIG. 25.

CP211-234+AF231-254 28/04/98 IVR
glucose/maltose vs galactose/maltose
sample CP214



40/63

FIG. 26.



41/63

FIG. 27.

C. albicans library screening experiment 15/12/97
glucose vs galactose
genom. sample 222g

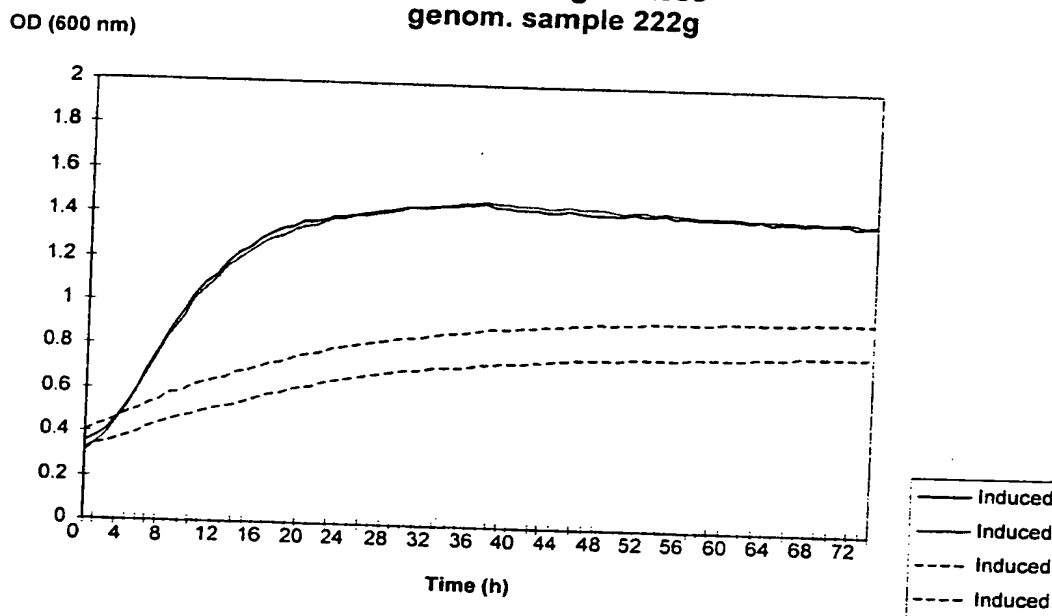
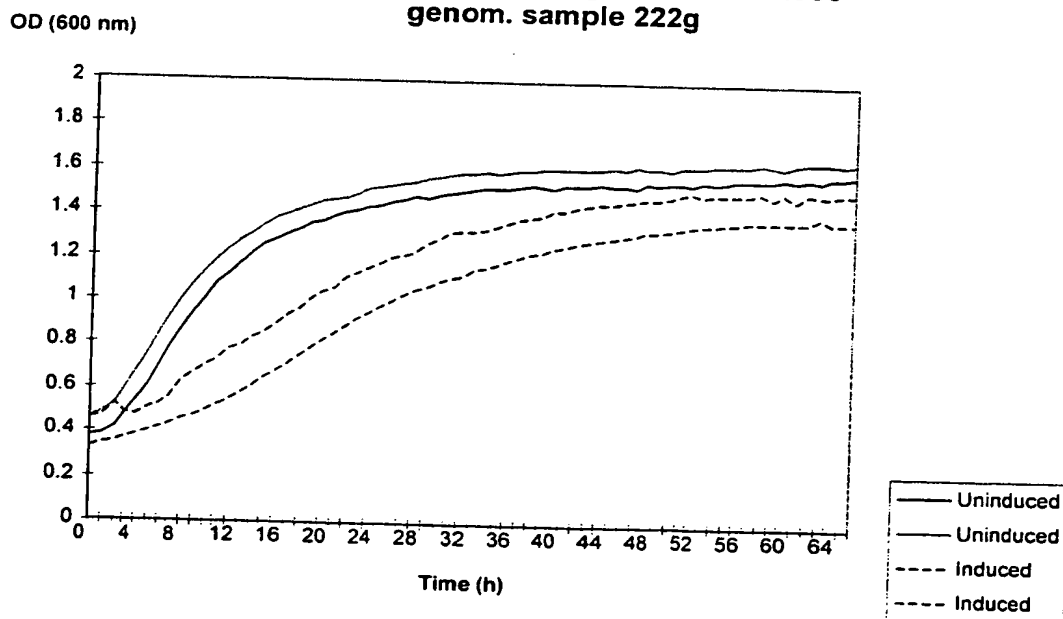


FIG. 28.

C. albicans library screening experiment 19/12/97
glucose/maltose vs galactose/maltose
genom. sample 222g

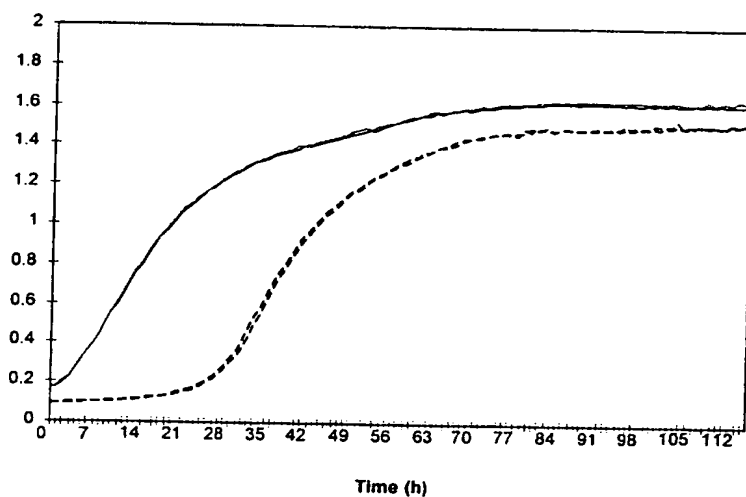


42/63

FIG. 29.

CP211-234+AF231-254 28/04/98
glucose/maltose vs galactose/maltose
sample CP223

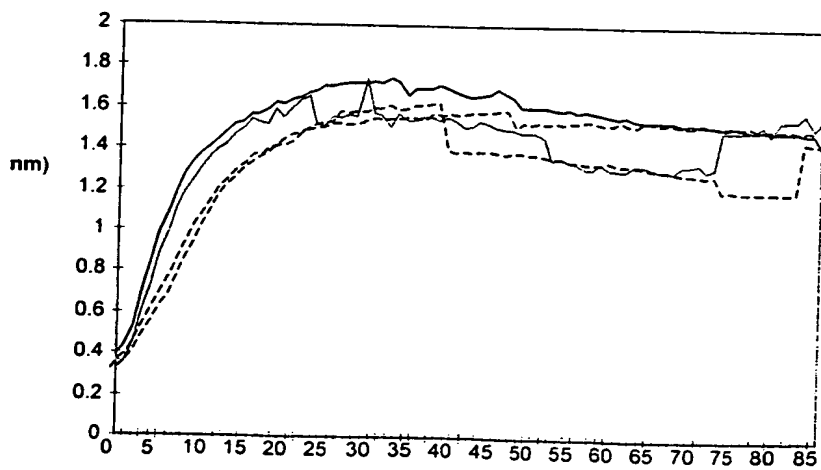
OD (600 nm)



— Uninduced
— Uninduced
- - - Induced
- - - Induced

FIG. 30.

C. albicans library screening experiment 24/04/98
glucose/maltose vs galactose/maltose
sample 226af



— Uninduced
— Uninduced
- - - Induced
- - - Induced

43/63

FIG. 31.

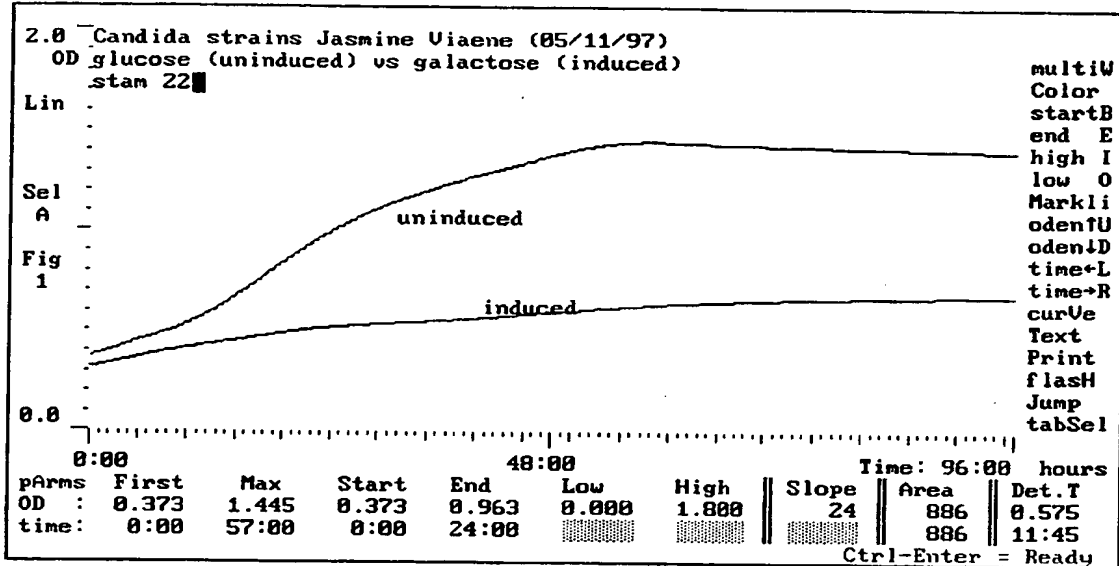
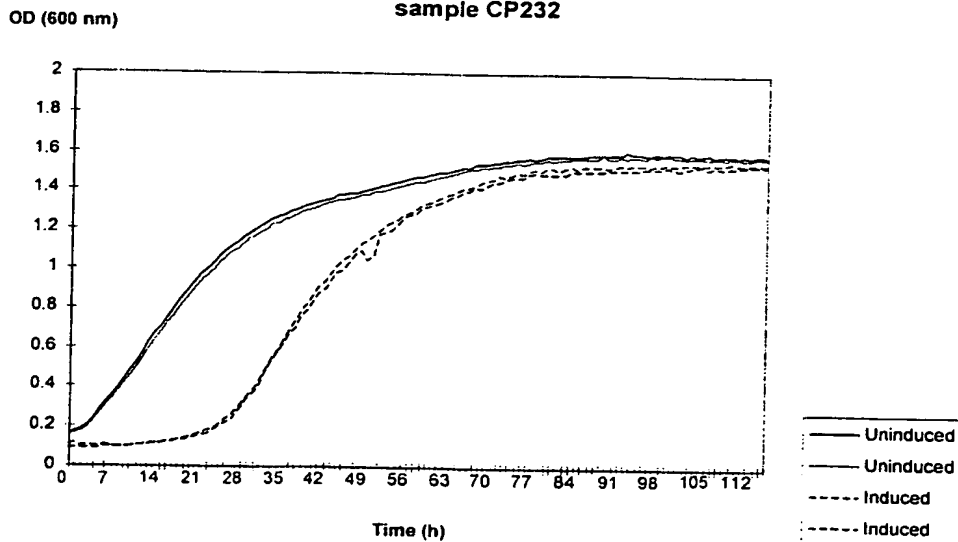


FIG. 32.

CP211-234+AF231-254 28/04/98
 glucose/maltose vs galactose/maltose
 sample CP232



44/63

FIG. 33.

CP211-234+AF231-254 28/04/98
glucose/maltose vs galactose/maltose
sample CP233

OD (600 nm)

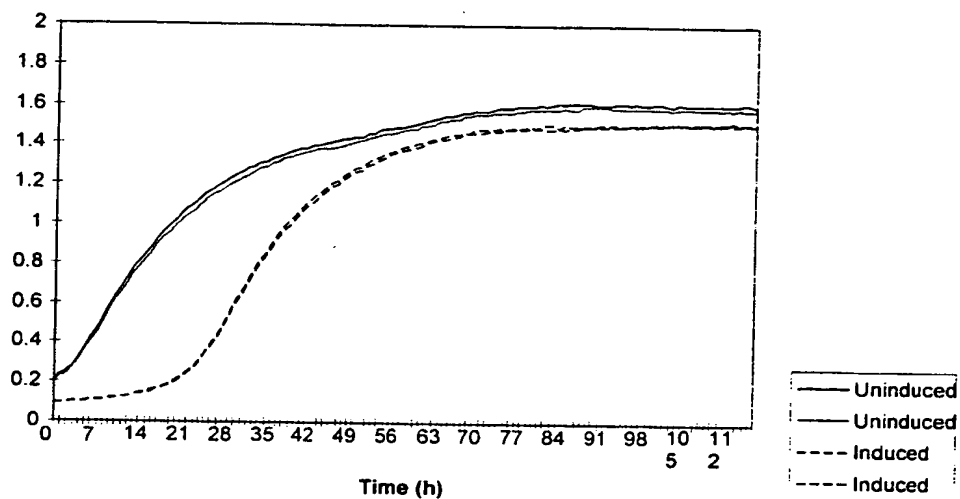
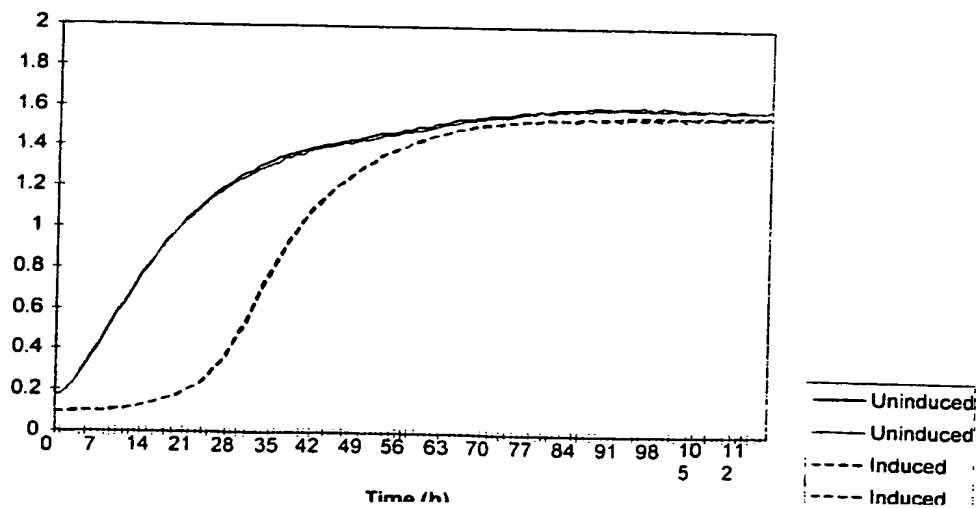


FIG. 34.

CP211-234+AF231-254 28/04/98 IVR
glucose/maltose vs galactose/maltose
sample AF249

OD (600 nm)



45/63

FIG. 35.

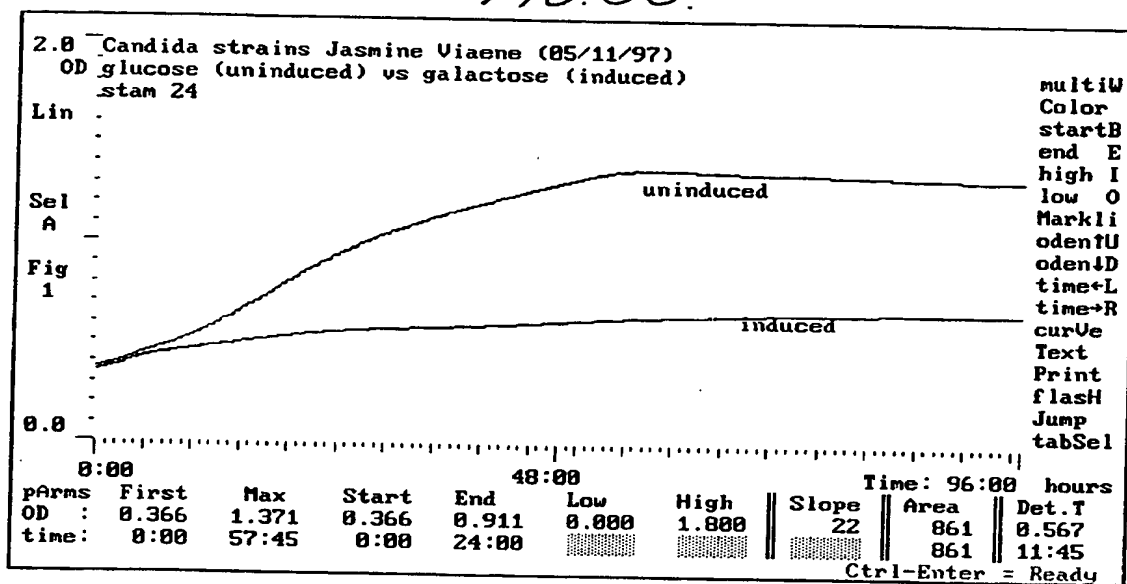
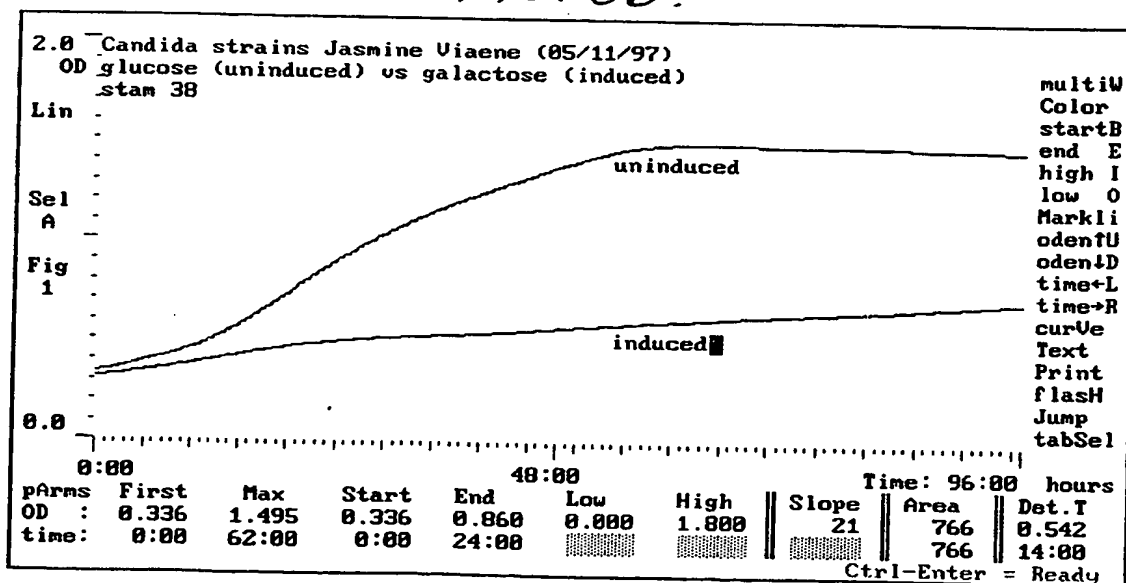


FIG. 36.



46/63

FIG. 37.

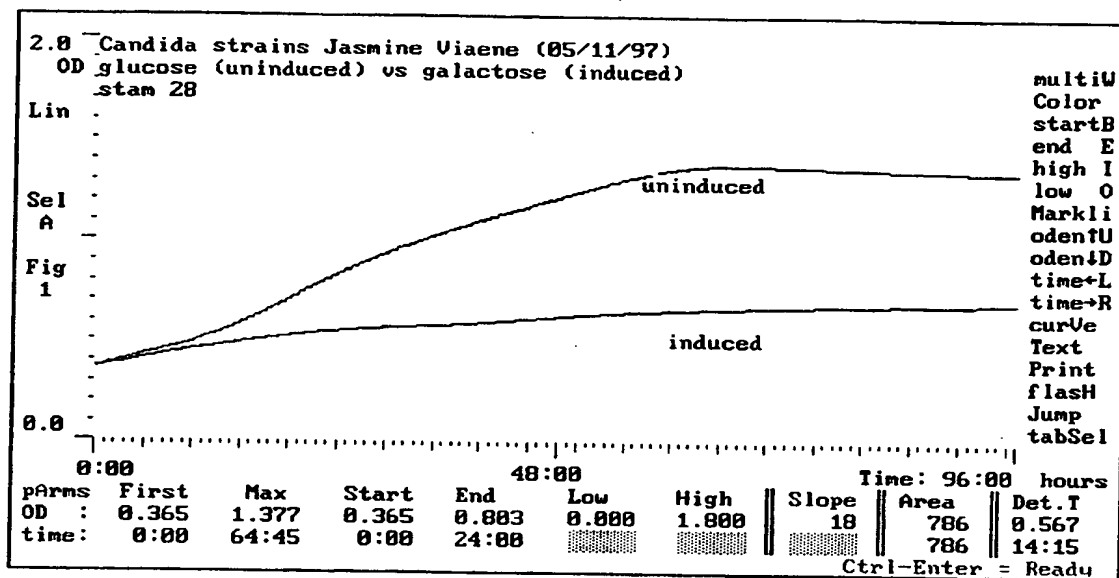
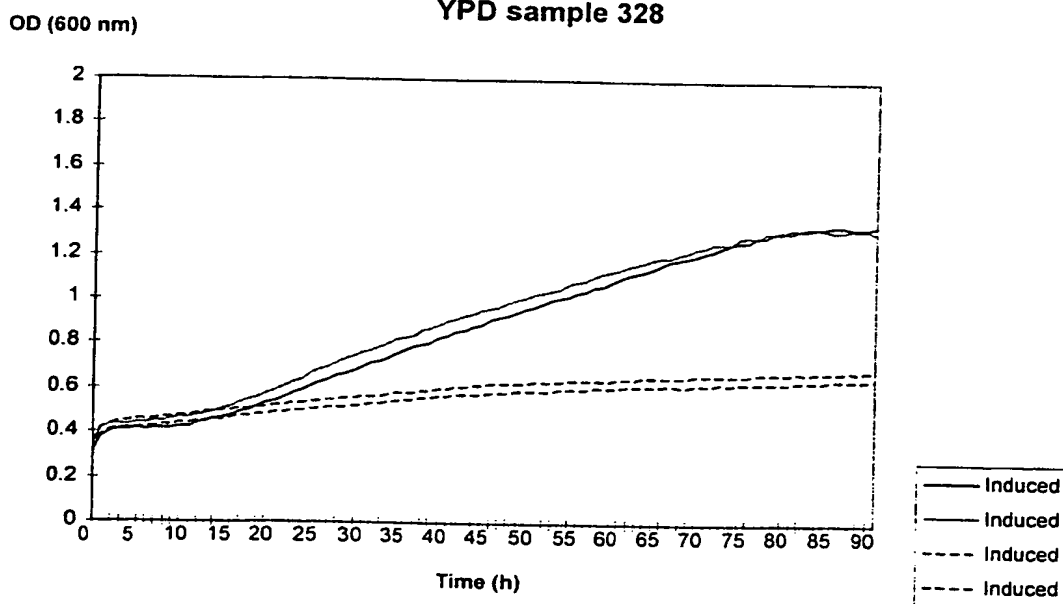


FIG. 38.

C. albicans library screening experiment 27/10/97
glucose vs galactose
YPD sample 328



47/63

FIG. 39

C. albicans cDNA library screening 12-02-98
glucose/maltose vs galactose/maltose
YPD sample 357

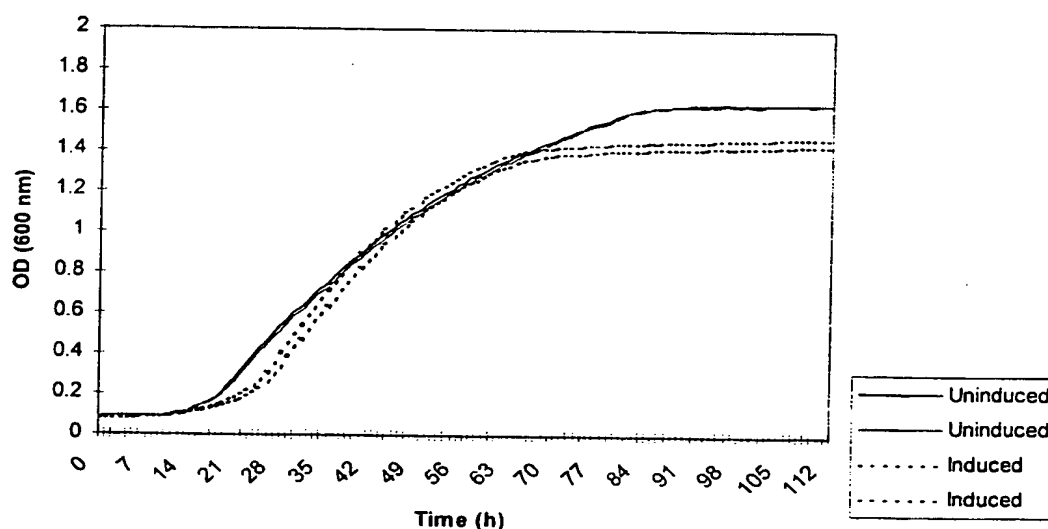
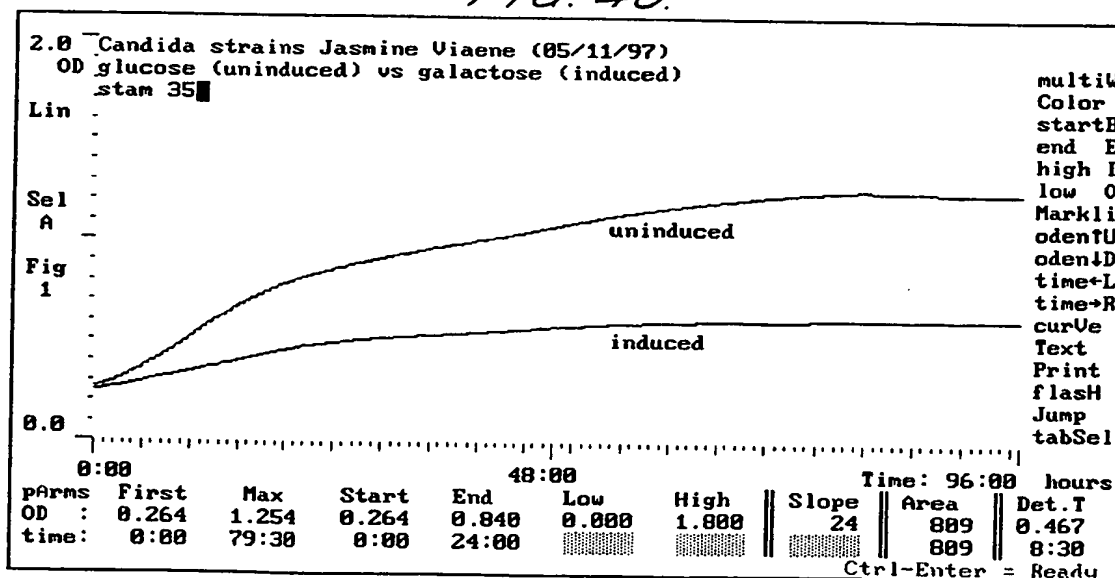


FIG. 40.



48/63

FIG. 41.

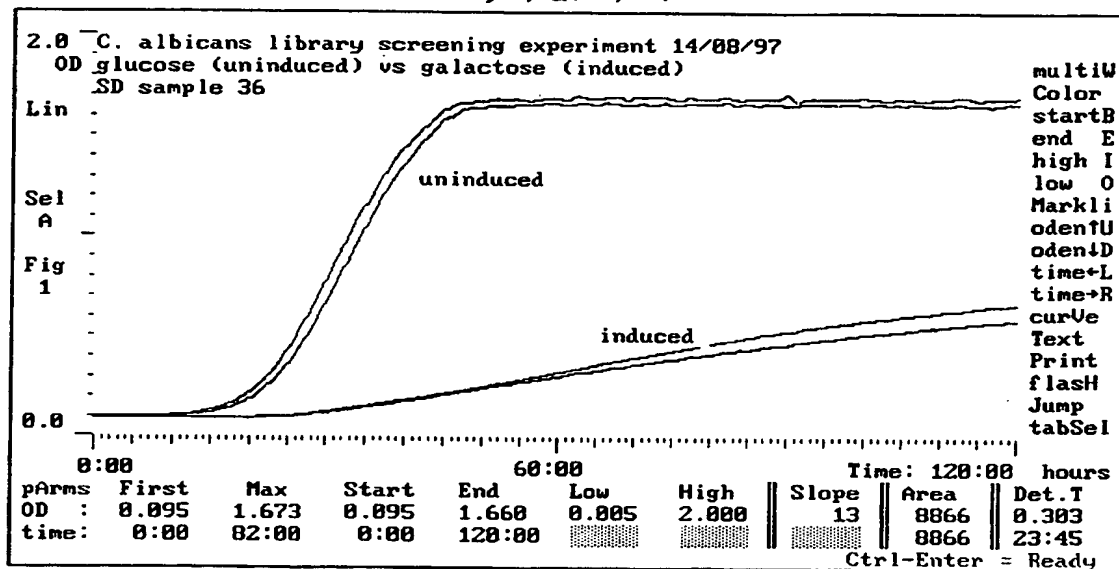
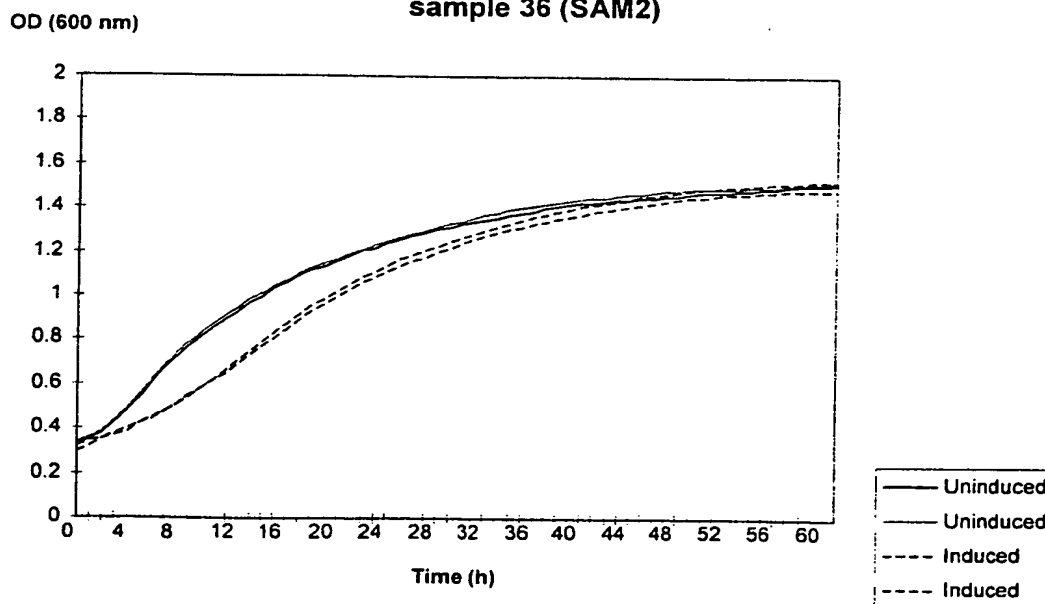


FIG. 42.

C. albicans library screening experiment 28/11/97
glucose/maltose vs galactose/maltose
sample 36 (SAM2)



49/63

FIG. 43.

C. albicans cDNA library screening 05/02/98
glucose/maltose vs galactose/maltose
YPD sample 360

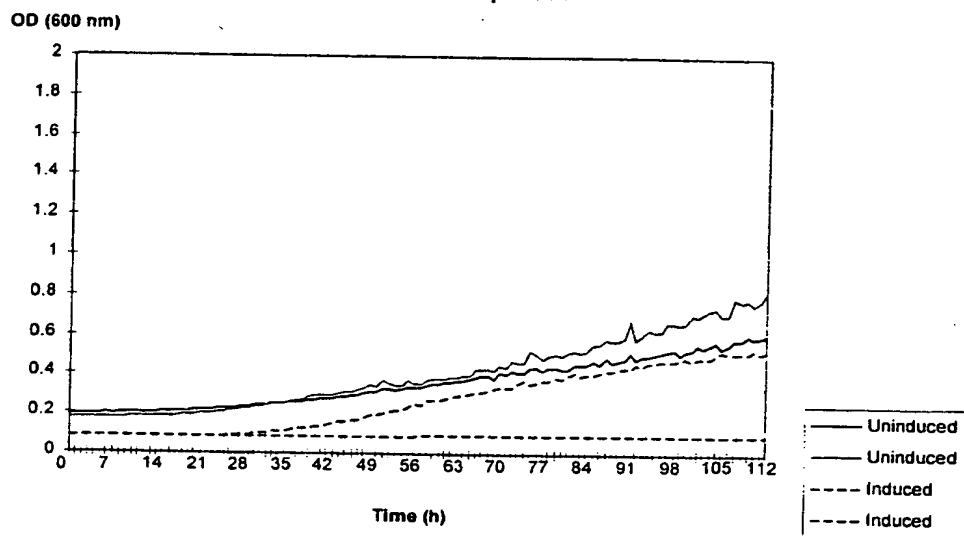
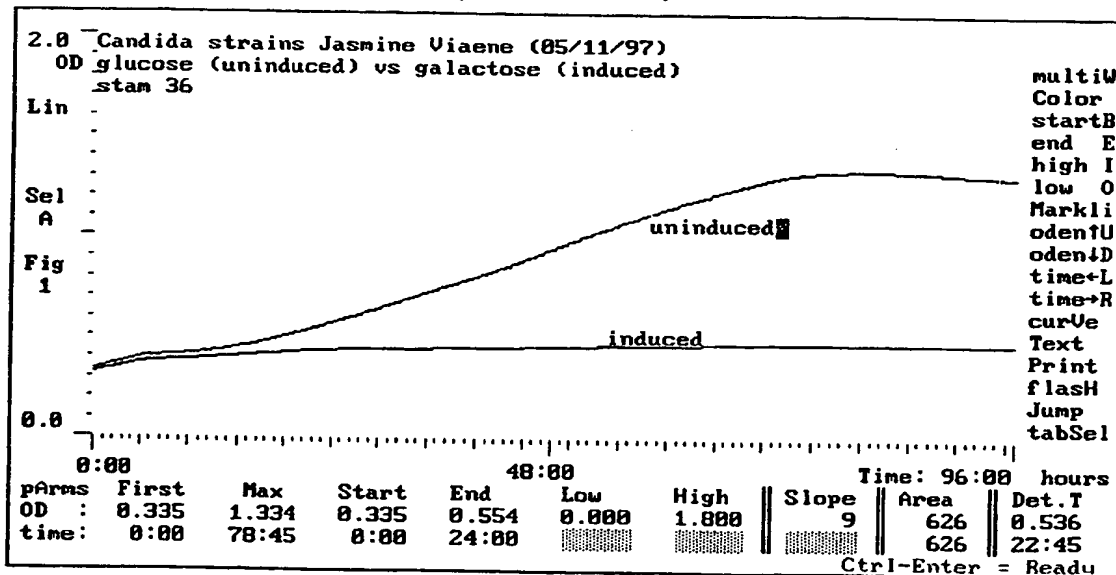


FIG. 44.



50/63

FIG. 45.

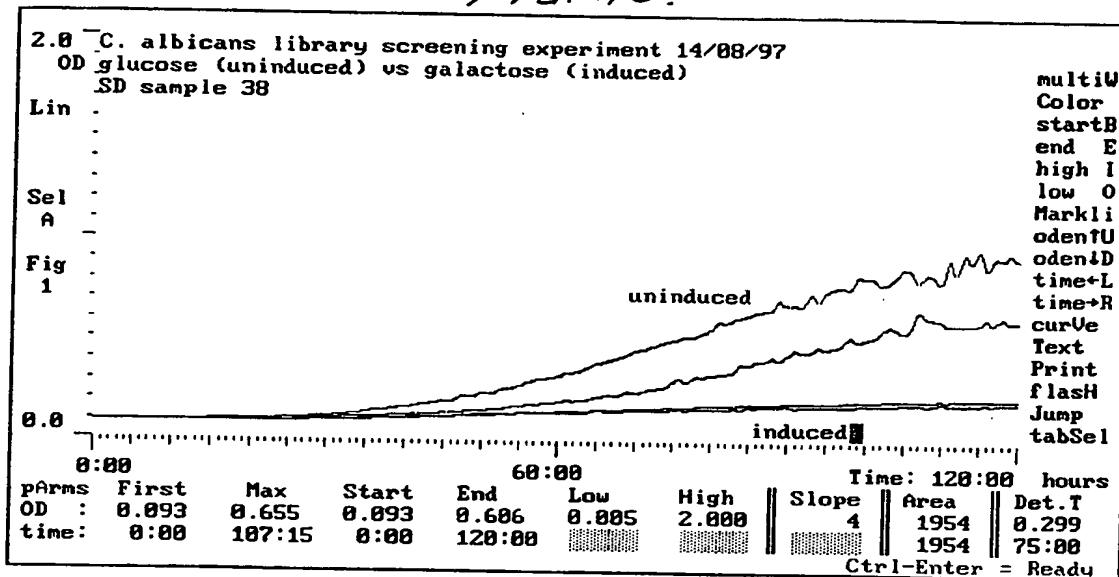
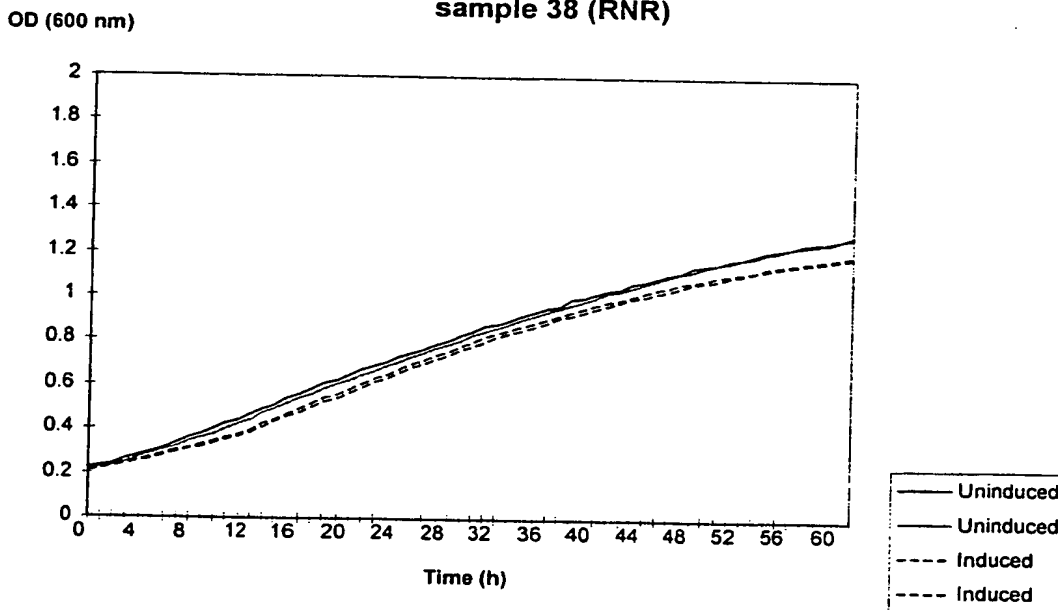


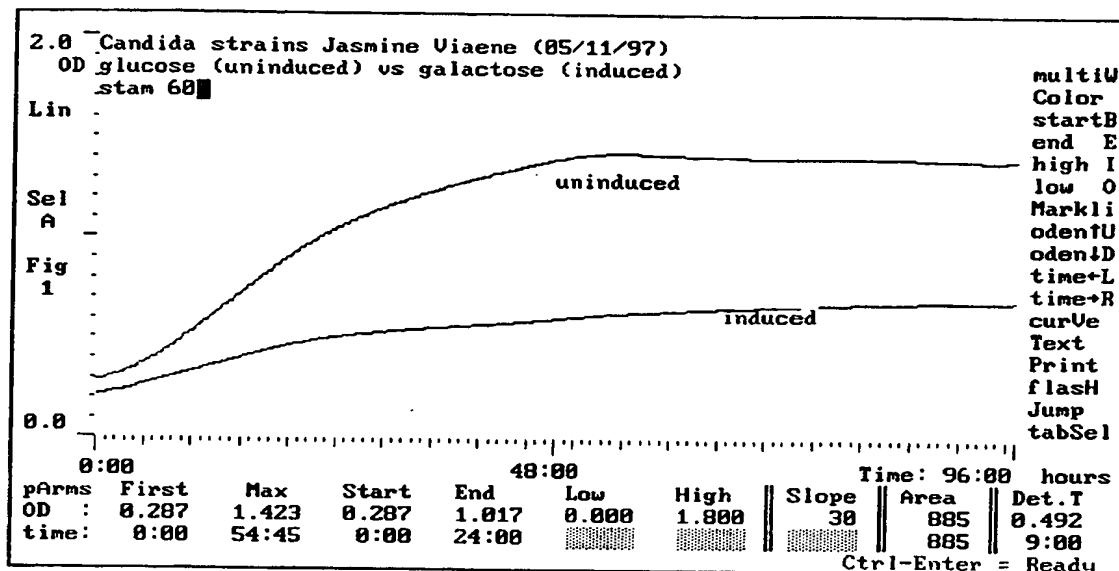
FIG. 46.

C. albicans library screening experiment 28/11/97
glucose/maltose vs galactose/maltose
sample 38 (RNR)



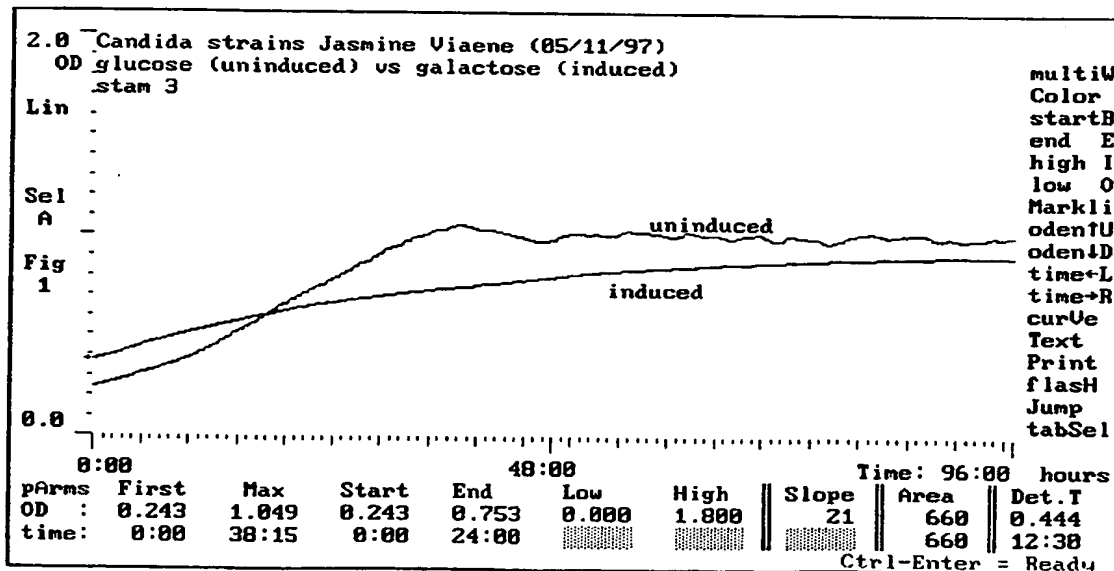
51/63

FIG. 47.



60gK (RAD18)

FIG. 48.



52/63

FIG. 49.

C. albicans cDNA library screening 12-02-98
glucose/maltose vs galactose/maltose
YPD sample 409

OD (600 nm)

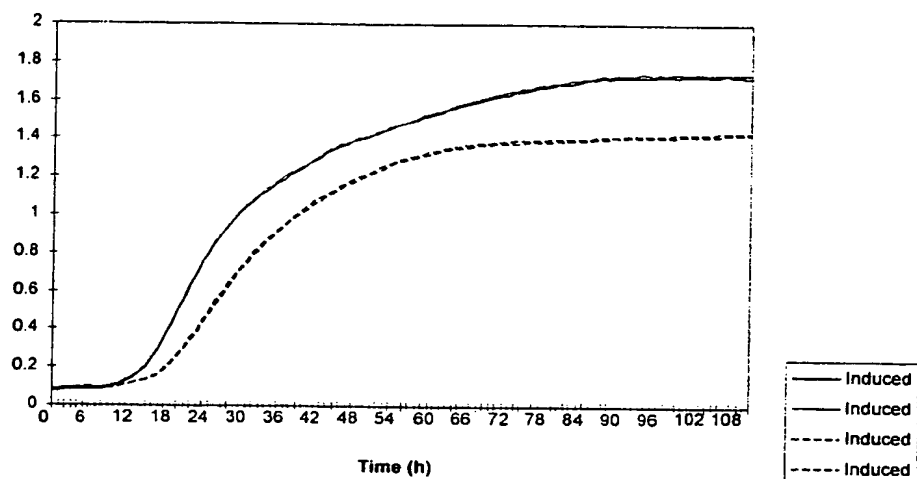
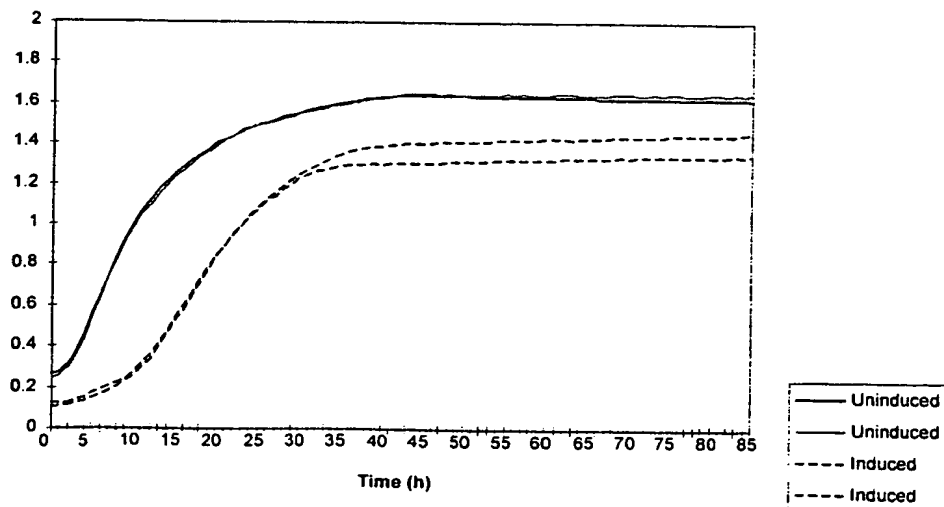


FIG. 50.

C. albicans library screening experiment 27/03/98
glucose/maltose vs galactose/maltose
sample 40AF

OD (600 nm)



53/63

FIG. 51.

C. albicans library screening experiment 17/03/98
glucose/maltose vs galactose/maltose
SD sample 485c

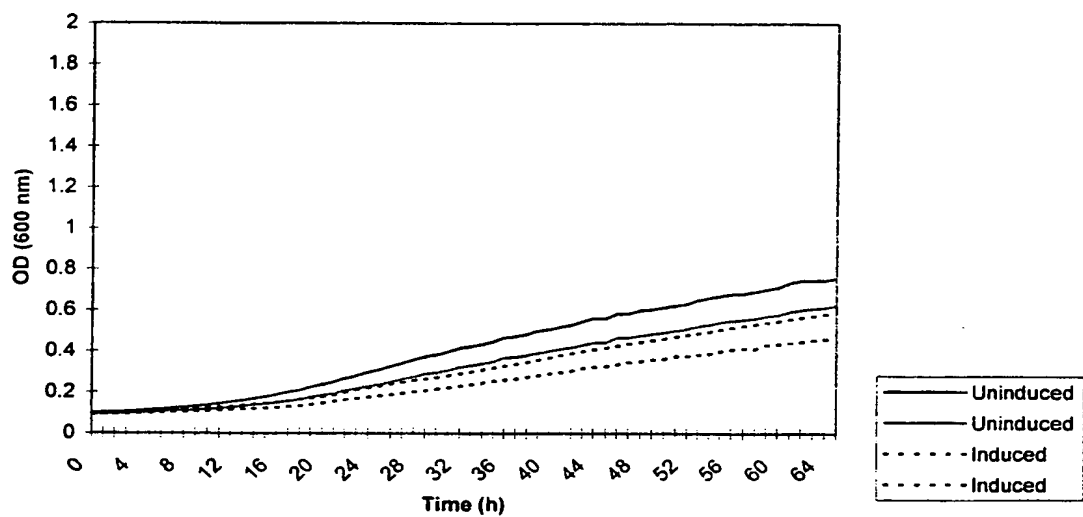
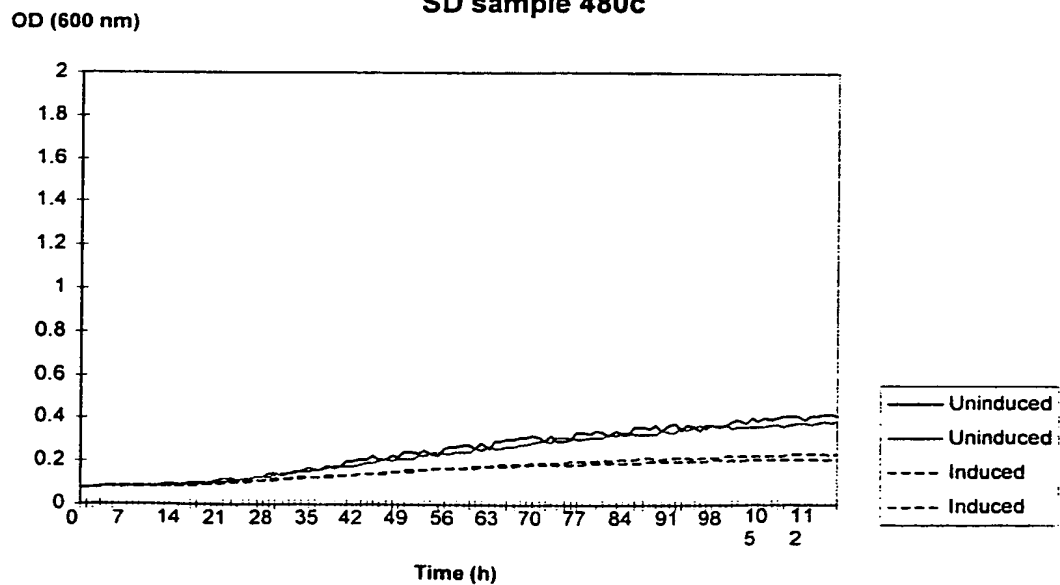


FIG. 52.

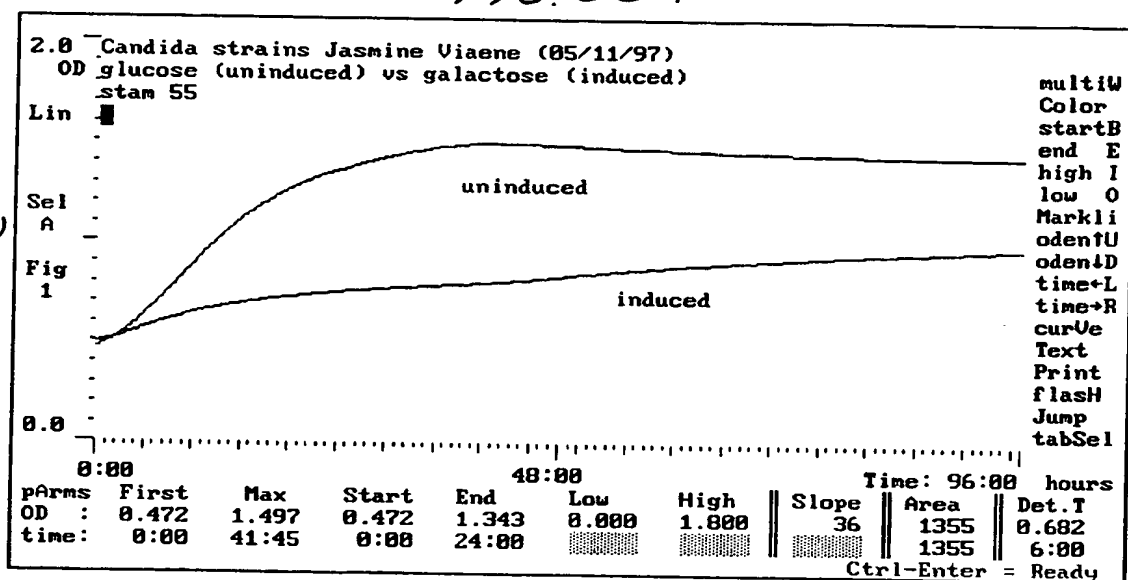
C. albicans cDNA library screening 10-03-98
glucose vs galactose
SD sample 480c



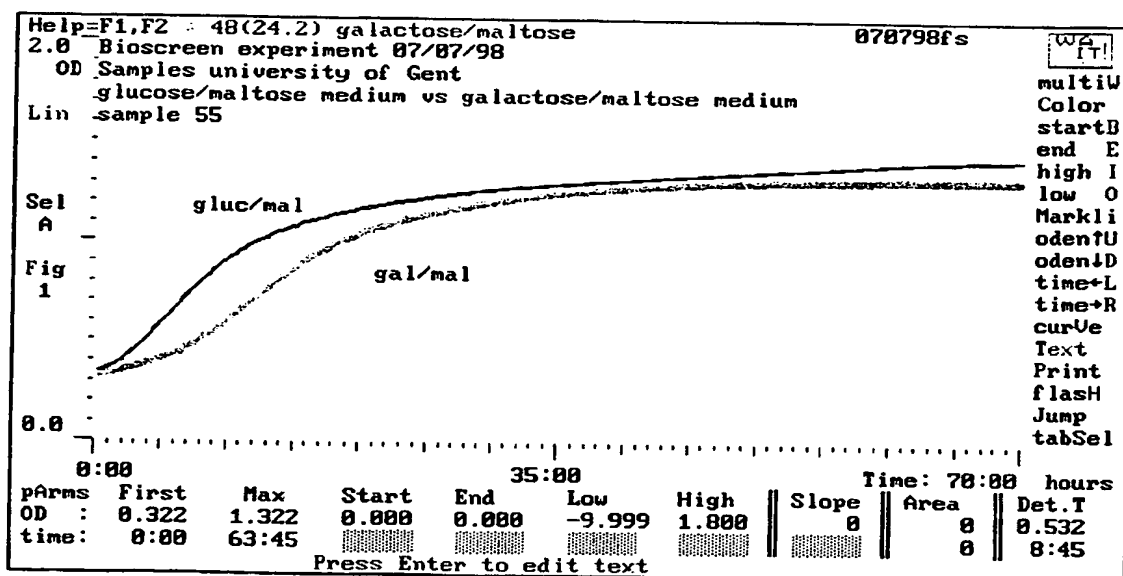
54/63

FIG. 53.

(a)



(b)



55/63

FIG. 54

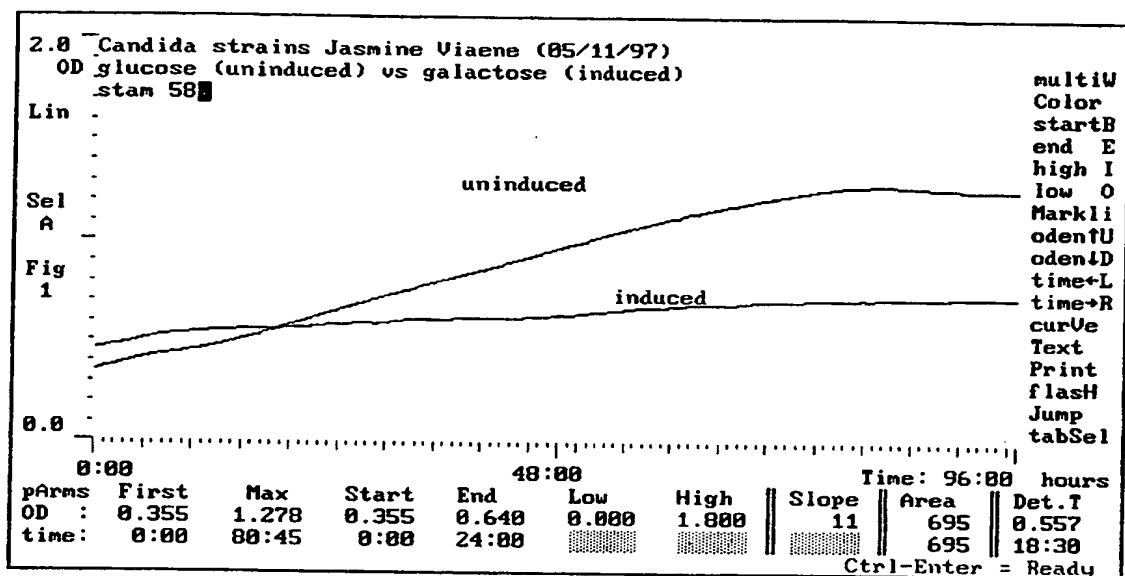
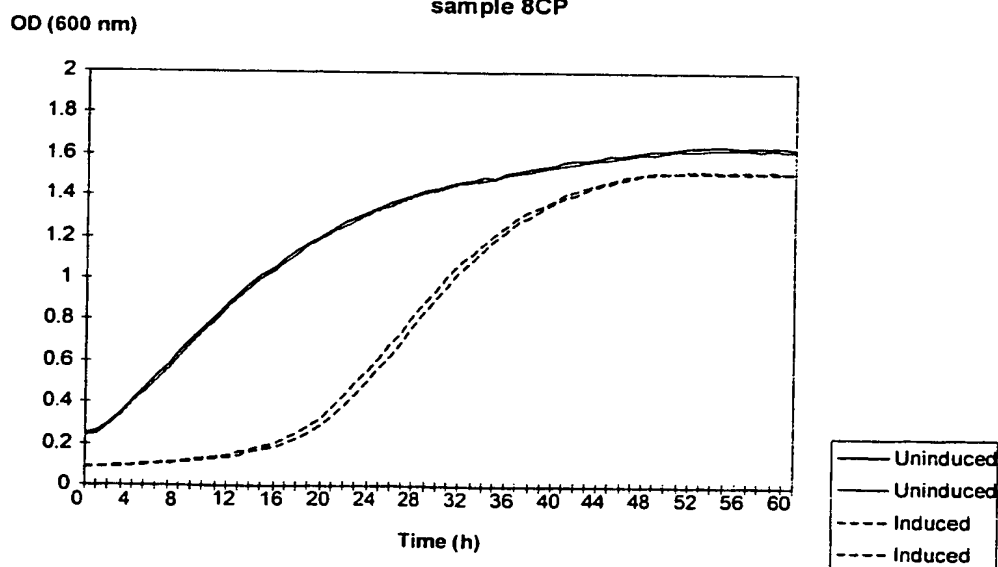


FIG. 55.

C. albicans library screening experiment 31/03/98
 glucose/maltose vs galactose/maltose
 sample 8CP



56/63

FIG. 56.

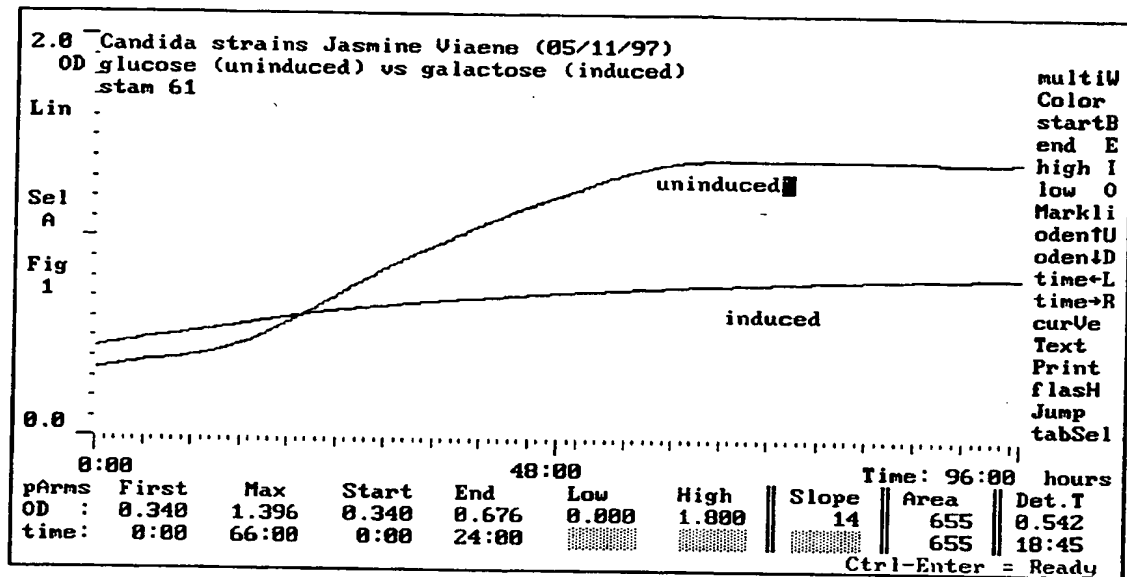
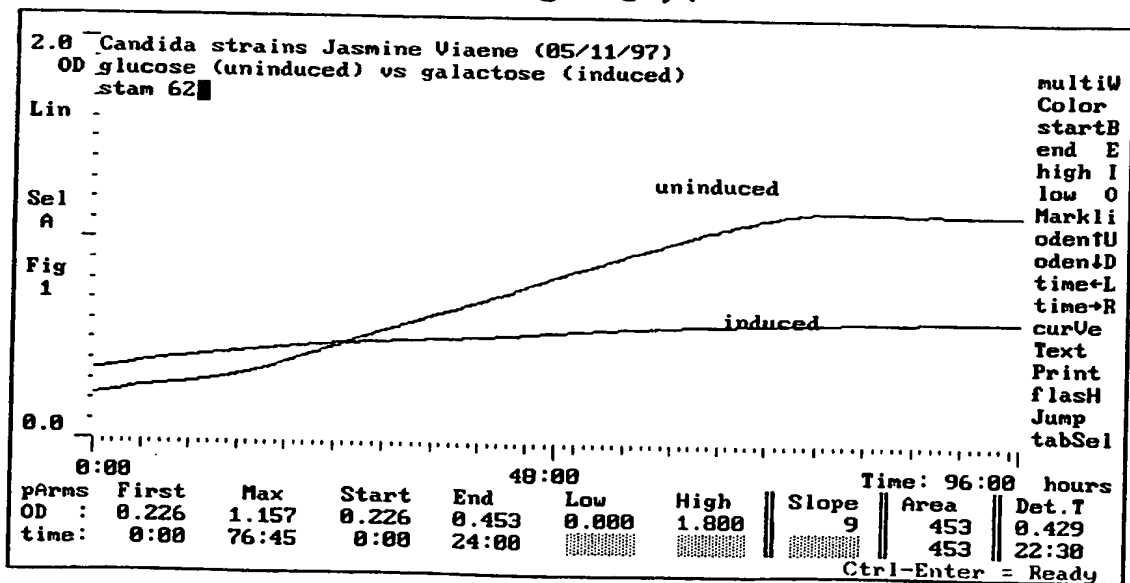


FIG. 57.



57/63

FIG. 58.

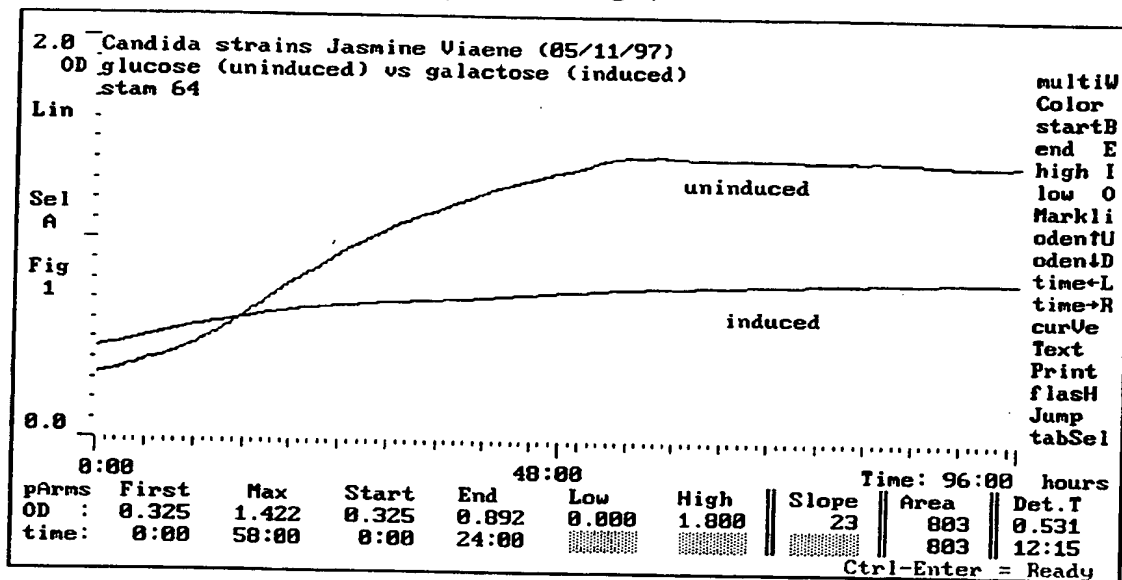
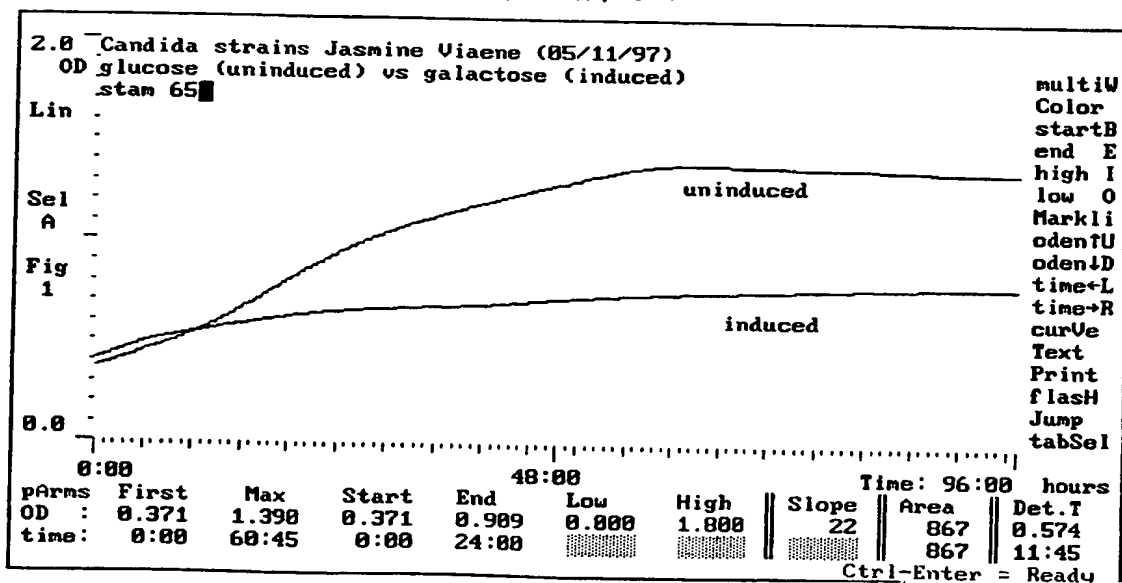


FIG. 59.



58/63

FIG. 60.

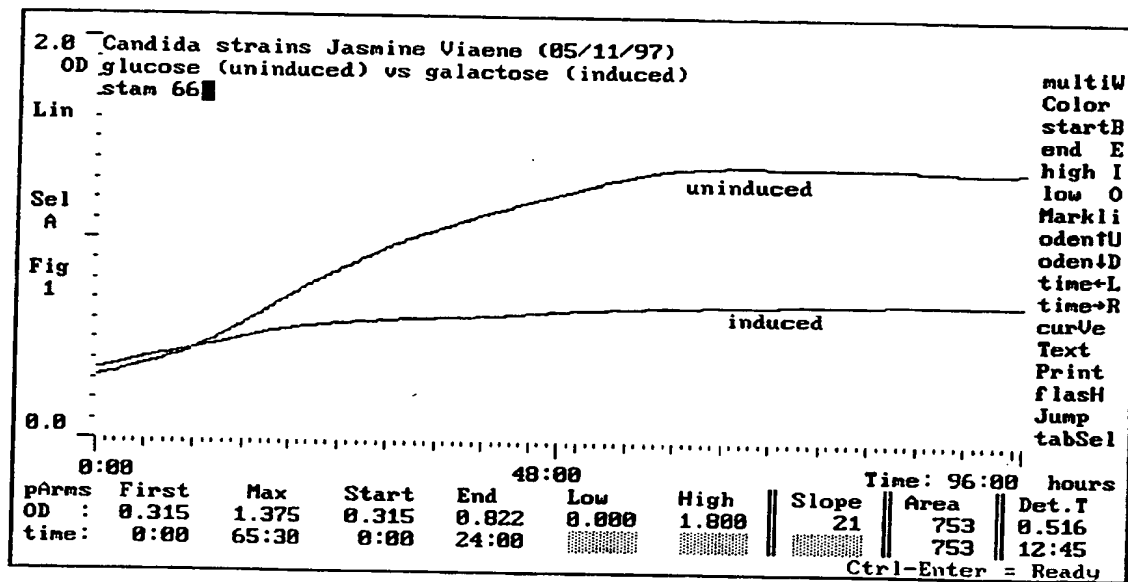
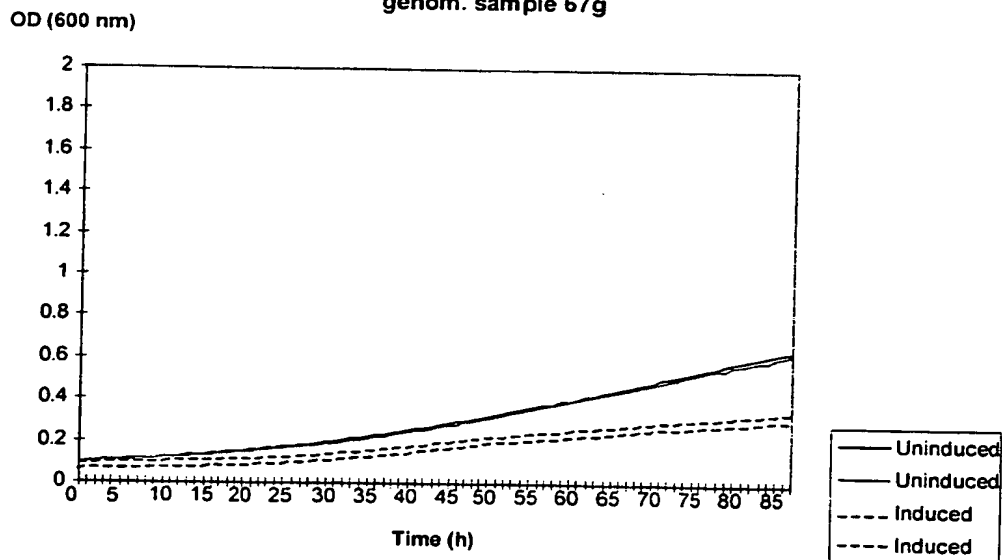


FIG. 61.

C. albicans library screening experiment 21/11/97
 glucose vs galactose
 genom. sample 67g



59/63

FIG. 62.

C. albicans library screening experiment 21/11/97
glucose vs galactose
genom. sample 80g

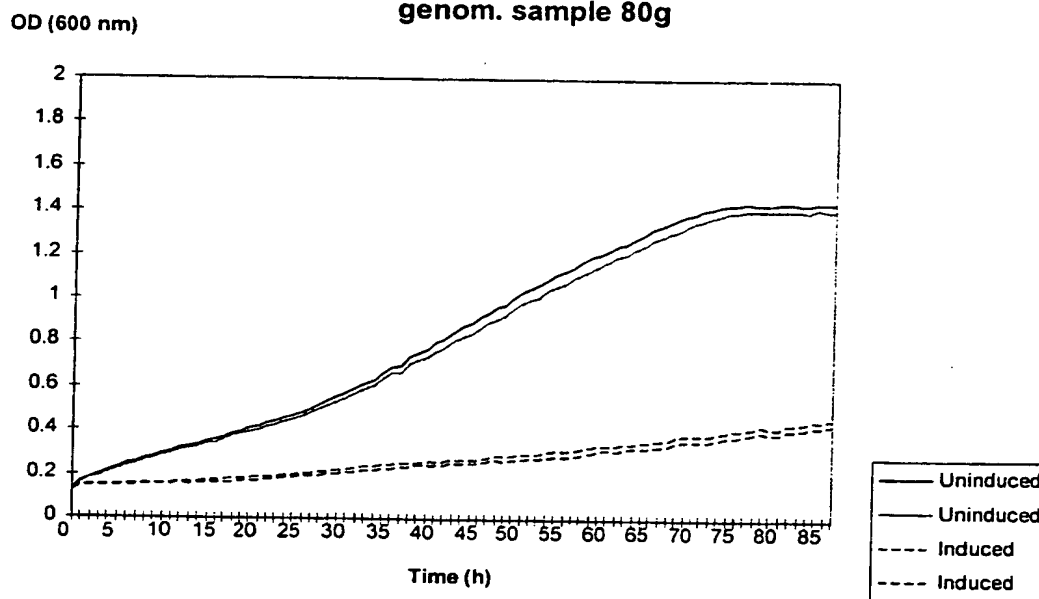
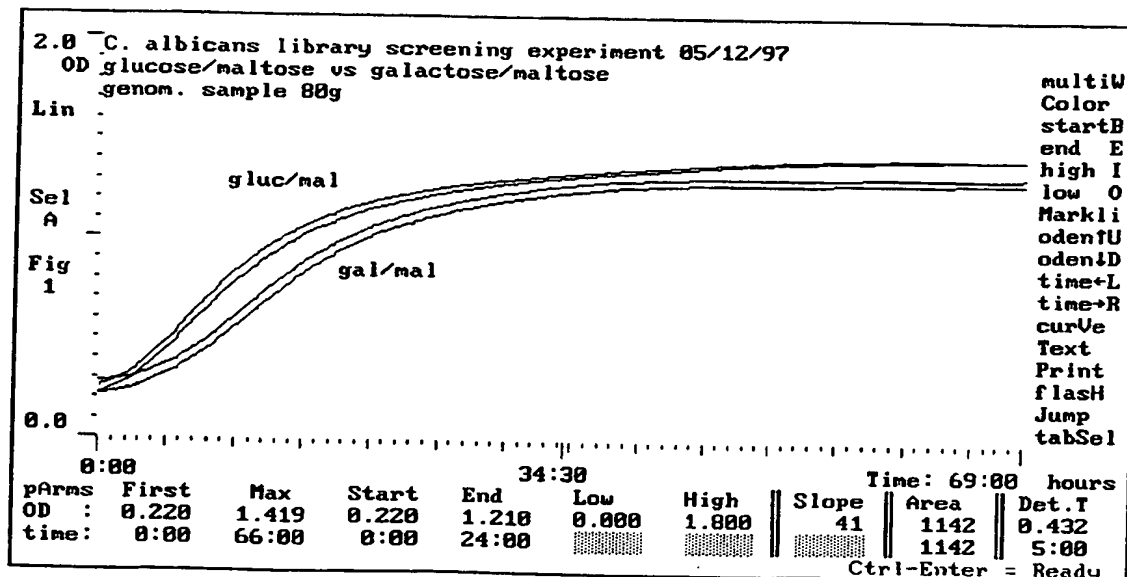
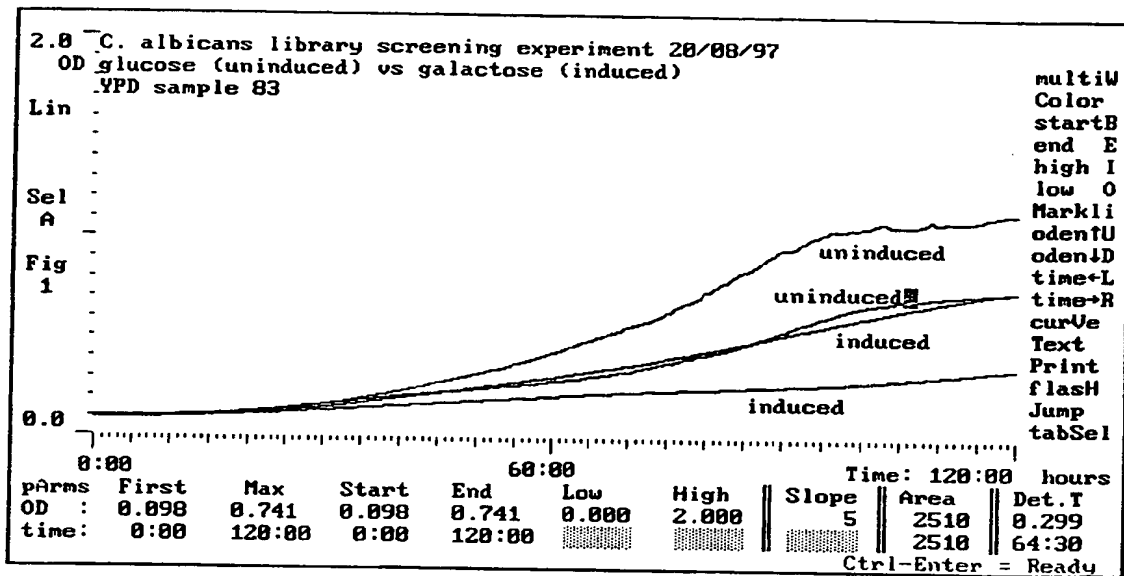


FIG. 63.



60/63

FIG. 6A.



83c3 (SHA3)

61/63

FIG. 65.

C. albicans library screening experiment 21/11/97
glucose vs galactose
genom. sample 85g

OD (600 nm)

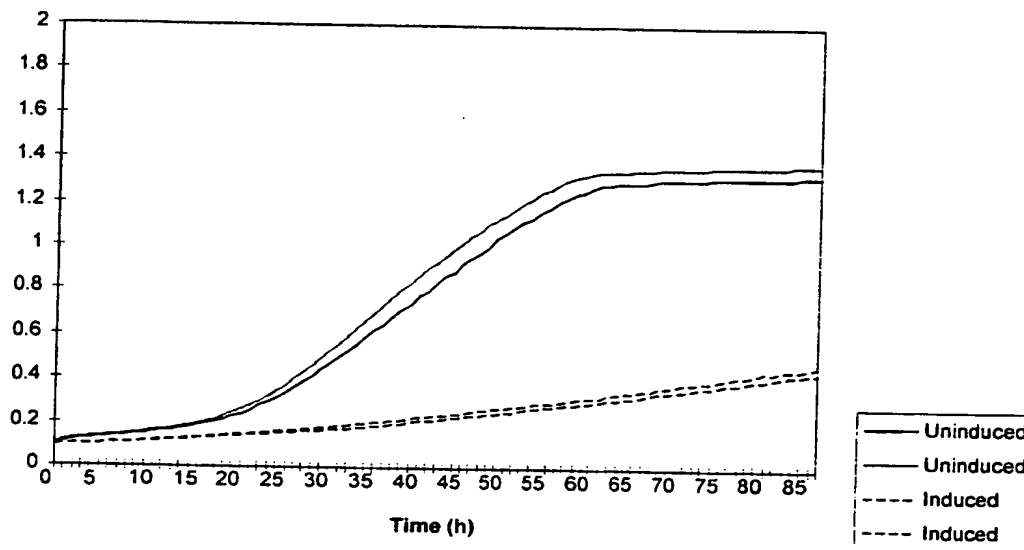
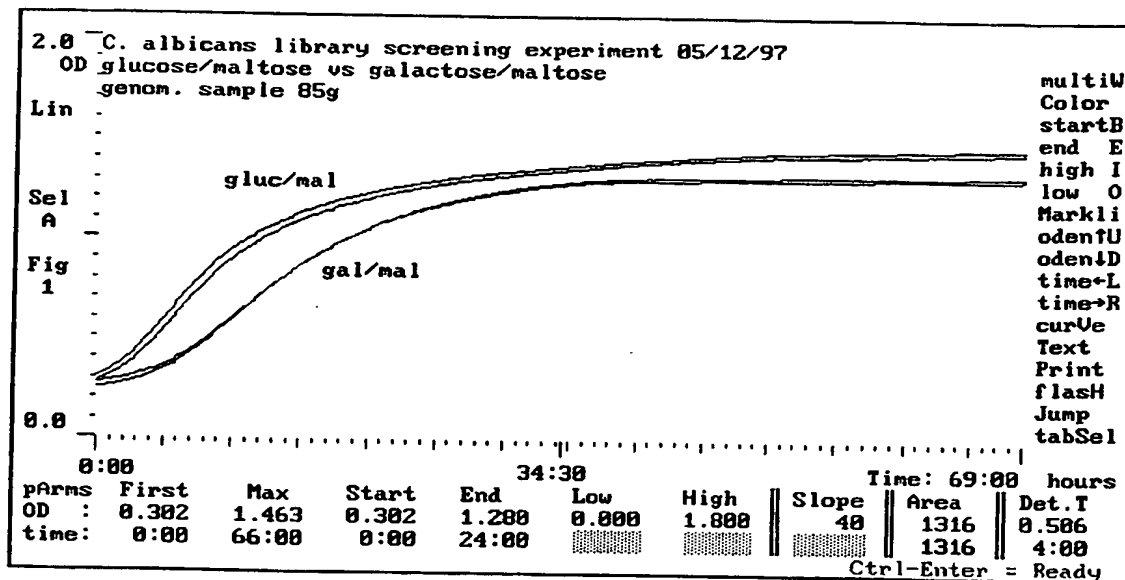


FIG. 66.



62/63

FIG. 67.

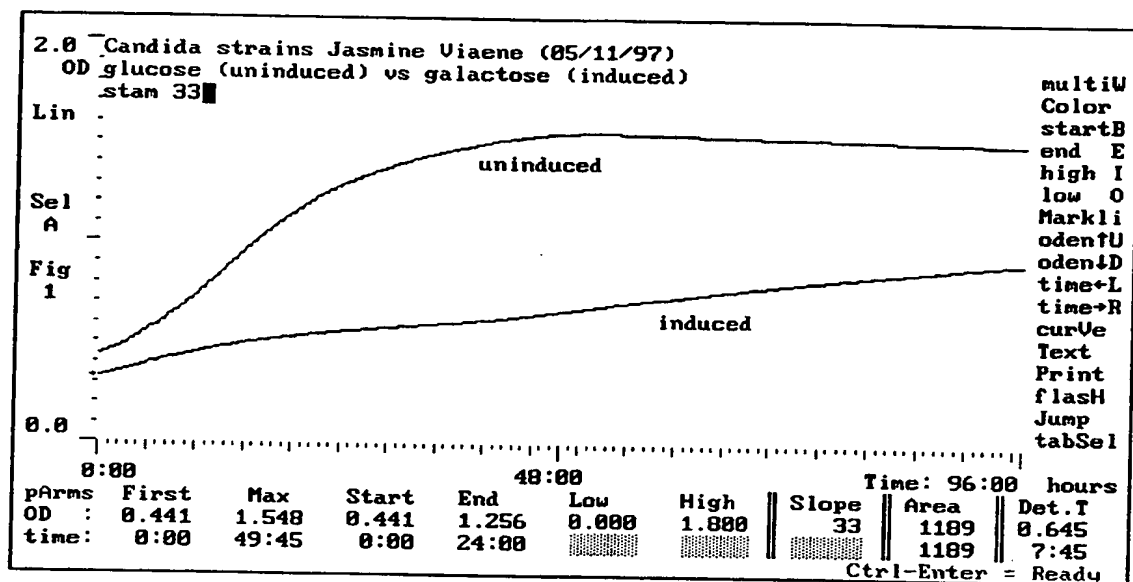
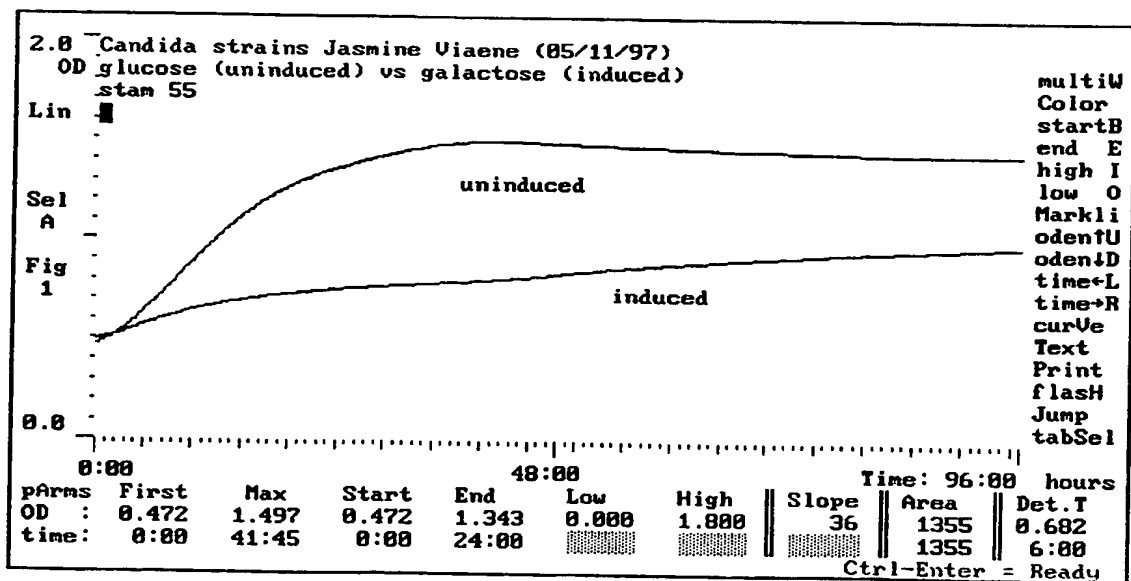


FIG. 68.



63/63

FIG. 69.

C. albicans library screening experiment 21/11/97
glucose vs galactose
genom. sample 99g

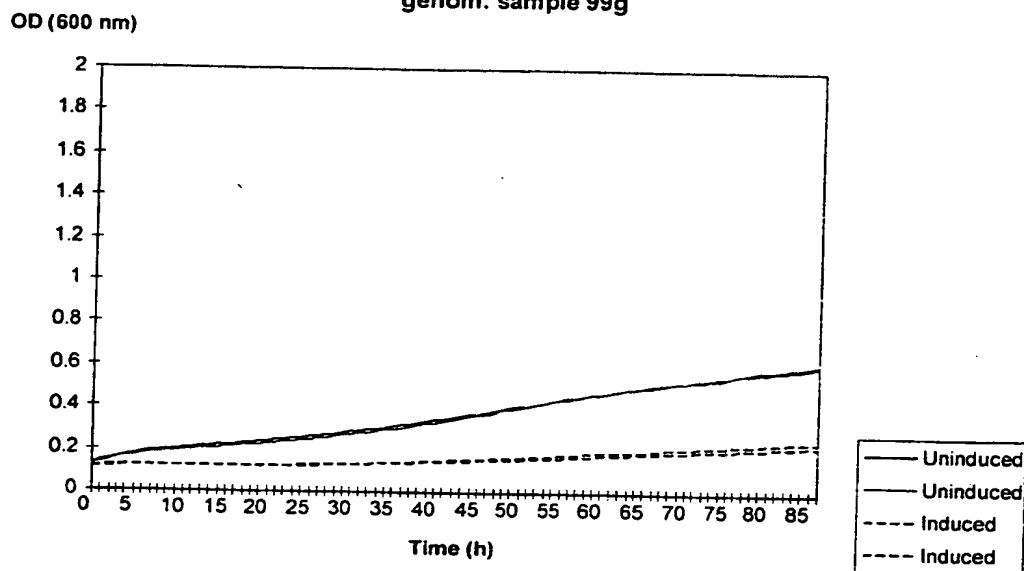
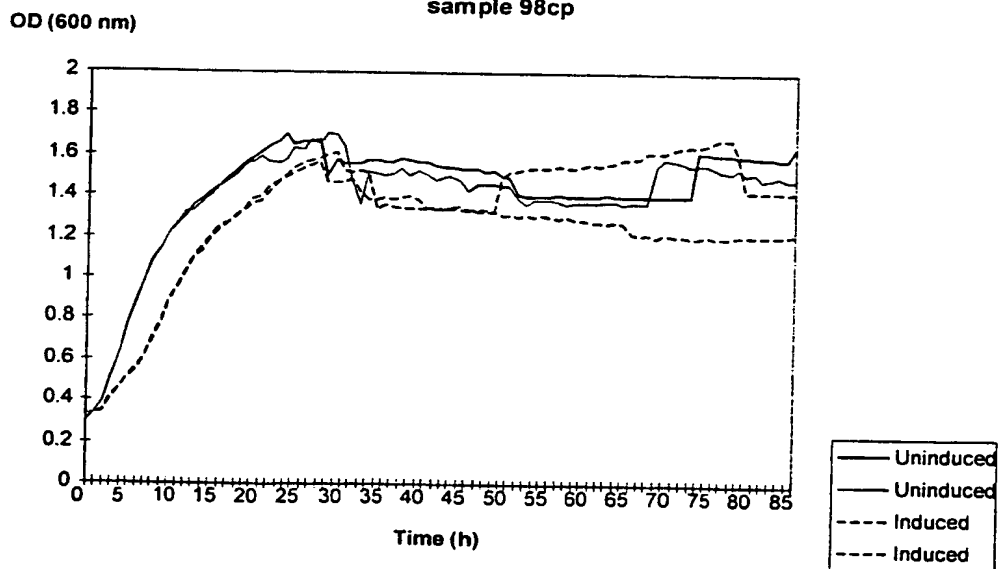


FIG. 70.

C. albicans library screening experiment 24/04/98
glucose/maltose vs galactose/maltose
sample 98cp



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<120> Drug Targets In Candida Albicans

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<212> PRT

<213> Candida albicans

<400> 4

Met His Phe Thr Ser Ser Leu Leu Ala Thr Leu Ile Trp Phe Thr Leu
 1 5 10 15

Pro Val Gln Ser Leu Asn Thr Glu Ser Arg Thr Thr Ser Asn Asn Thr
 20 25 30

Ile Ser Ile Leu Thr Asn His Phe Gln Ile Leu Lys Asp Leu Leu Pro
 35 40 45

Tyr Ser Lys Thr Ser Lys Pro Gln Ile Lys Glu Ser Arg Pro Leu Ile
 50 55 60

Lys Val Ser Arg Asp Gly Val Pro Ile Asn Phe His Arg Ala Pro Ala
 65 70 75 80

Ile Ile Met Lys Ser Asn Lys Thr Asp Asp Leu Val Arg Asn Ser Asn
 85 90 95

Lys Thr Met Val Leu Thr Glu Ile Lys Thr Ile Thr Glu Phe Ala Thr
 100 105 110

Thr Thr Val Ser Pro Thr Gln Glu Phe Gln Ala Leu Gln Ile Asn Leu
 115 120 125

Asn Thr Leu Ser Ile Glu Thr Ser Thr Pro Thr Phe Gln Ser His Asp
 130 135 140

Phe Pro Pro Ile Thr Ile Glu Asp Thr Pro Lys Thr Leu Glu Pro Glu
 145 150 155 160

Glu Ser Ser Asp Ala Leu Gln Arg Asp Ala Phe Asp Gln Ile Lys Lys
 165 170 175
 Leu Glu Lys Leu Val Leu Asp Leu Arg Leu Glu Met Lys Glu Gln Gln
 180 185 190
 Lys Ser Phe Asn Asp Gln Leu Val Asp Ile Tyr Thr Ala Arg Ser Ile
 195 200 205
 Val Pro Ile Tyr Thr Thr His Ile Val Thr Ser Ala Ile Pro Ser Tyr
 210 215 220
 Val Pro Lys Glu Glu Val Met Val Ser His Asp Thr Ala Pro Ile Val
 225 230 235 240
 Ser Arg Pro Arg Thr Asp Ile Pro Val Ser Gln Arg Ile Asp Thr Ile
 245 250 255
 Ser Lys His Lys Met Asn Gly Lys Asn Ile Leu Asn Asn Asn Pro Pro
 260 265 270
 Pro Asn Ser Val Leu Ile Val Pro Gln Phe Gln Phe His Glu Arg Met
 275 280 285
 Ala Thr Lys Thr Glu Val Ala Tyr Met Lys Pro Lys Ile Val Trp Thr
 290 295 300
 Asn Phe Pro Thr Thr Thr Ala Thr Ser Met Phe Asp Asn Phe Ile Leu
 305 310 315 320
 Lys Asn Leu Val Asp Glu Thr Asp Ser Glu Ile Asp Ser Gly Glu Thr
 325 330 335
 Glu Leu Ser Asp Asp Tyr Tyr Tyr Tyr Tyr Ser Tyr Glu Asp Asp Gly
 340 345 350
 Lys Glu Asp Asp Ser Asp Glu Ile Thr Ala Gln Ile Leu Leu Ser Asn
 355 360 365
 Ser Glu Leu Gly Thr Lys Thr Pro Asn Phe Glu Asp Pro Phe Glu Gln
 370 375 380
 Ile Asn Ile Glu Asp Asn Lys Val Ile Ser Val Asn Thr Pro Lys Thr
 385 390 395 400
 Lys Lys Pro Thr Thr Thr Val Phe Gly Thr Ser Thr Ser Ala Leu Ser
 405 410 415

Thr Phe Glu Ser Thr Ile Phe Glu Ile Pro Lys Phe Phe Tyr Gly Ser
 420 425 430

Arg Arg Lys Gln Ser Ser Ser Phe Lys Asn Lys Asn Ser Thr Ile Lys
 435 440 445

Phe Asp Val Phe Asp Trp Ile Phe Glu Ser Gly Thr Thr Asn Glu Lys
 450 455 460

Val His Gly Leu Val Leu Val Ser Ser Gly Val Leu Leu Gly Thr Cys
 465 470 475 480

Leu Leu Phe Ile Leu
 485

<210> 5

<211> 2193

<212> DNA

<213> Candida albicans

<400> 5

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 cgagaagatc atgaaaaatt taaagagatc aatatagcat atgaaacaat tagagattat 180
 tatcaagaga atgggcaaaa gaacagtcaa cggatcccta acacaaacac agagcataat 240
 tcccatcaaa aaccacatta taacactggc ccttattcca catatcgttt tacgacctca 300
 tctaccacga ctgataatac caatcacact ggacattcaa gttctcggtt tacttattat 360
 aatttccacc aaaaagcgca agagaataac cgcaaacaag atgaagaaag ggcagcccaa 420
 cgtgaacgat taaaaaagga gctcttccag aggcaacaag cggaagaagc acaacgaaag 480
 aaggaatttg aacaaaaggc cgaattcatc aaagcatcat tacttgaaat gcgccaaga 540
 gaaatagaga ggcggaaaca gcaaaaaggaa agggaacaaa gacaaaagga gcacgaagca 600
 aagagggata tcaggataca acaactttca gagcaggatt cacggagtaa tcaaactaaa 660
 gaagaagagg aagtgttcaa gaaggcccg tctactaatt cgggagcaga cgagactggg 720
 ttgatgtcag ataaagagtt tgatgattct gcatattcac ccgattatgt gtttgaagag 780
 aatttgtgga ataaaccaa tcatccagat acaaatacata aaaccaaaaa atatactgag 840
 aatgtgggtg aaaatctaga ttctccacca aatgatacat ctgcgtacaa ttcaagtttt 900
 catgatgaaa ctaatatcca aaatgagatc caaataccag aaaatgacga gtatgtacca 960
 cagatgaaag ctacatccag tgtcaataat accaccatcc ctgcacaaaag aagacatgag 1020
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 caggacaata gtacatatat tcctcagggg tctttaggac acgaatttag aaatatatttg 1260
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 ataattgatg ttgaagctta cgtacctgat gtcaaagcag caacttcaaa caccacccca 1440
 gcaacaggac aaacatcagc aaggtcggaa aaactgccac ccttacctac tcatattcca 1500

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aatccatcga ccatgaatga agctcgacct catccaacaa ctccacataa aagatcaaaa 1560
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tttaaggata tgtatgagag tttgcctgac cattcaagta aggcaacacc taaagacgat 1680
attttaaccc gttctaaaag aagactttat acatataccg atggaacatc aaaggctgaa 1740
acgttatcta caccaatgaa caaaaatcct gttcgtggac atagtaccaa gaaaaagctt 1800
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caaagtcaaa ttgatccttc tgtttccaag caagtgtggg ctaaatacgt tgatgcaatc 1920
ttgacttatc aaagagaatt tttcaattat aaaaaagtga ttgttcaata ccaaattggaa 1980
cggataaaca aagaccttga acattttgac gatataaatg atgggttcaca cactgagaat 2040
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gcgttacgac aatttggtac gaccattgcc acgtatcagc aaaacctcca gtgggttaac 2160
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<210> 6

<211> 730

<212> PRT

<213> Candida albicans

<400> 6

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Met Gln Pro Thr Val Gln His Phe Lys Ile Leu Gly Ile Ser Pro Thr
  1                      5                      10                      15

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Ser Thr Leu Asp Glu Ile Arg Arg Ala Tyr Arg Lys Leu Ser Leu Arg
          20                      25                      30

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Tyr His Pro Asp Lys Thr Pro Arg Arg Glu Asp His Glu Lys Phe Lys
      35                      40                      45

```

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Glu Ile Asn Ile Ala Tyr Glu Thr Ile Arg Asp Tyr Tyr Gln Glu Asn
      50                      55                      60

```

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Gly Gln Lys Asn Ser Gln Pro Ile Pro Asn Thr Asn Thr Glu His Asn
      65                      70                      75                      80

```

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Ser His Gln Lys Pro His Tyr Asn Thr Gly Pro Tyr Ser Thr Tyr Arg
          85                      90                      95

```

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Phe Thr Thr Ser Ser Thr Thr Thr Asp Asn Thr Asn His Thr Gly His
          100                      105                      110

```

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Ser Ser Ser Arg Phe Thr Tyr Tyr Asn Phe His Gln Lys Ala Gln Glu
      115                      120                      125

```

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Asn Asn Arg Lys Gln Asp Glu Glu Arg Ala Ala Gln Arg Glu Arg Leu
      130                      135                      140

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Lys Lys Glu Leu Phe Gln Arg Gln Gln Ala Glu Glu Ala Gln Arg Lys
      145                      150                      155                      160

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Lys Glu Phe Glu Gln Lys Ala Glu Phe Ile Lys Ala Ser Leu Leu Glu
 165 170 175
 Met Arg Arg Arg Glu Ile Glu Arg Arg Lys Gln Gln Lys Glu Arg Glu
 180 185 190
 Gln Arg Gln Lys Glu His Glu Ala Lys Arg Asp Ile Arg Ile Gln Gln
 195 200 205
 Leu Ser Glu Gln Asp Ser Arg Ser Asn Gln Thr Lys Glu Glu Glu Glu
 210 215 220
 Val Phe Lys Lys Ala Arg Ser Thr Asn Ser Gly Ala Asp Glu Thr Gly
 225 230 235 240
 Leu Met Ser Asp Lys Glu Phe Asp Asp Ser Ala Tyr Ser Pro Asp Tyr
 245 250 255
 Leu Phe Glu Glu Asn Leu Trp Asn Lys Pro Asn His Pro Asp Thr Asn
 260 265 270
 His Lys Thr Lys Lys Tyr Thr Glu Asn Val Val Glu Asn Leu Asp Ser
 275 280 285
 Pro Pro Asn Asp Thr Ser Ala Tyr Asn Ser Ser Phe His Asp Glu Thr
 290 295 300
 Asn Ile Gln Asn Glu Ile Gln Ile Pro Glu Asn Asp Glu Tyr Val Pro
 305 310 315 320
 Gln Met Lys Ala Thr Ser Ser Val Asn Asn Thr Thr Ile Pro Ala Gln
 325 330 335
 Arg Arg His Glu Ser Leu Ser Thr Ser Glu Asn Lys Arg Arg Lys Phe
 340 345 350
 Glu Thr Ala Asp Val Gly Val Asp Gly Leu Asp Ser Pro Val Arg Ala
 355 360 365
 Gln Pro Glu Ile Ser Gly Lys Ser Lys Ser Pro Ile Ile Pro Asp Val
 370 375 380
 Ile Leu Leu Ser Asp Glu Glu Thr Glu Thr Pro Glu Ala Asn Ala Val
 385 390 395 400
 Gln Asp Asn Ser Thr Tyr Ile Pro Gln Gly Ser Leu Gly His Glu Phe
 405 410 415

Arg Asn Ile Leu Glu Glu His Pro Arg Gln Val Lys Asn Lys Gln Asn
 420 425 430
 Ser Gly Val Ala Phe Ala Phe Pro Asn Ala Ser Lys Asn Thr Glu Asn
 435 440 445
 Lys Leu His Ser Asn Phe Lys Asp Lys Asp Glu Gly Ile Ile Asp Val
 450 455 460
 Glu Ala Tyr Val Pro Asp Val Lys Ala Ala Thr Ser Asn Thr Thr Pro
 465 470 475 480
 Ala Thr Gly Gln Thr Ser Ala Arg Ser Glu Lys Ser Pro Pro Leu Pro
 485 490 495
 Thr His Ile Pro Asn Pro Ser Thr Met Asn Glu Ala Arg Pro His Pro
 500 505 510
 Thr Thr Pro His Lys Arg Ser Lys Val Ile Phe Asp Leu Lys Asp Leu
 515 520 525
 Glu Gln Lys Leu Gly Asn Asp Ile Glu Asp Leu Asp Phe Lys Asp Met
 530 535 540
 Tyr Glu Ser Leu Pro Asp His Ser Ser Lys Ala Thr Pro Lys Asp Asp
 545 550 555 560
 Ile Leu Thr Arg Ser Lys Arg Arg Leu Tyr Thr Tyr Thr Asp Gly Thr
 565 570 575
 Ser Lys Ala Glu Thr Leu Ser Thr Pro Met Asn Lys Asn Pro Val Arg
 580 585 590
 Gly His Ser Thr Lys Lys Lys Leu Ser Met Leu Asp Met His Ala Ser
 595 600 605
 Ser Lys Ile Gln Ser Leu Leu Pro Pro Gln Pro Pro Gln Met Ser Ile
 610 615 620
 Asp Pro Ser Val Ser Lys Gln Val Trp Ala Lys Tyr Val Asp Ala Ile
 625 630 635 640
 Leu Thr Tyr Gln Arg Glu Phe Phe Asn Tyr Lys Lys Val Ile Val Gln
 645 650 655
 Tyr Gln Met Glu Arg Ile Asn Lys Asp Leu Glu His Phe Asp Asp Ile
 660 665 670

Asn Asp Gly Ser His Thr Glu Asn Leu Asp Thr Phe Lys His Cys Leu
 675 680 685

Glu Gln Asp Tyr Leu Val Met Ser Glu Phe Asn Glu Ala Leu Arg Gln
 690 695 700

Phe Gly Thr Thr Ile Ala Thr Tyr Gln Gln Asn Leu Gln Trp Val Asn
 705 710 715 720

Thr Phe Met Glu Arg Asp Pro Asn Trp Leu
 725 730

<210> 7

<211> 50

<212> PRT

<213> Candida albicans

<400> 7

Met Asn Ser Ala Phe Cys Ser Asn Ser Phe Phe Arg Cys Ala Ser Ser
 1 5 10 15

Ala Cys Cys Leu Trp Lys Ser Ser Phe Phe Asn Arg Ser Arg Trp Ala
 20 25 30

Ala Leu Ser Ser Ser Cys Leu Arg Leu Phe Ser Cys Ala Phe Trp Trp
 35 40 45

Lys Leu
 50

<210> 8

<211> 61

<212> PRT

<213> Candida albicans

<400> 8

Met Tyr His Leu Val Glu Asn Leu Asp Phe Gln Pro His Ser Gln Tyr
 1 5 10 15

Ile Phe Trp Phe Tyr Asp Leu Tyr Ser Asp Asp Leu Val Tyr Ser Thr
 20 25 30

Asn Ser Leu Gln Thr Asn Asn Arg Val Asn Met Gln Asn His Gln Thr
 35 40 45

Leu Tyr Ser Thr Ser Asn Gln Ser Arg Ser Leu Pro Asn
 50 55 60

<210> 9

<211> 77

<212> PRT

<213> Candida albicans

<400> 9

Met Tyr Tyr Cys Pro Ala Gln His Leu Leu Gln Glu Phe Gln Ser Leu
 1 5 10 15

Arg Pro Val Lys Val Leu His Gln Gly Leu Ser Glu Thr Trp Ile Phe
 20 25 30

Gln Ile Phe Ser Val Val Pro Ala Ser Gly Asn Leu Thr His Gln Pro
 35 40 45

Gln Arg Arg Ser Phe Gln Ile Ser Phe Phe Cys Phe Gln Lys Trp Lys
 50 55 60

Val Thr His Val Phe Phe Val Gln Gly Trp Trp Tyr Tyr
 65 70 75

<210> 10

<211> 463

<212> DNA

<213> Candida albicans

<400> 10

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 ctaaattact tcacagagcc tttactacct taatttaaga ttatctattg tttctgttct 180
 tttgcaatca ccttgactcg tttttttttc agccagtttt ttcgtaaaat ctgaccaaaa 240
 atttacaact ctaattttaa actctaaata acaattaaaa ctcaattcag acaagtcctt 300
 ctgctcattc tgagtcttct ctattgtctt ttgacttttt gtgtgtgact attttcatga 360
 tcaccccggt tcttgcatth ttttcagtca actttttctc aaaatcaagc caaaaaaaca 420
 catttaactg cctatacaac gcaaacctat tcaaaacaag gtt 463

<210> 11

<211> 582

<212> DNA

<213> Candida albicans

<400> 11

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gatttgttgt tgaagaaaag tgaccaccta gttttttctg ccaacatttt ttgcatgag 120
 ccgtcgacgc gttgtctttt tctacccac gtttaacaat cttgccagtc aattccctag 180
 ccaaataaac tttagactca caactctaac actgactcgt gccccctgt ttaaactcta 240
 aattacttca cagagccttt actaccttaa ttttaagatta tctattgttt ctgttttttt 300
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 ctcatctga gtcttctcta ttgtcttttg actttttgtg tgtgactatt ttcgatgaca 480
 ccccgtttct tgcatttttt tcagtcaact ttttctcaaa atcaagccaa aaaaacacac 540
 ctttaactac ctatacaacg caaacctatt caaaacaagg tt 582

<210> 12

<211> 1066

<212> DNA

<213> Candida albicans

<400> 12

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 tgctcgatgg acaaatttat cagaaacaac atttatattg actccaaaat catcaattgc 180
 tgwttatagt attagaattt tcacttctgg tgggaatgaa ttaccatttg ctggcatcc 240
 tacttttaggt actgcatttg cattattgga agatggtaaa ataaaaccaa atgacaatgg 300
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 taataatagt aatgagttgc cgtttttgtt atcttttgaa ttaccatatt tcaaatttca 420
 tgaaattgat gacaaagtaa tcgaggaatt acaacattca tggaatggaa ccaatattat 480
 tggtaaaccg gtacttattg atgctgggtcc aaaatgggca gttttccaac ttggctccgg 540
 taaagaagta ttagacttga atgytgattt agcacaaatt gagagattaa gtttagaaaa 600
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 cacttgctcc tggagtagtt tgatctaatt gatgtaattt atttaataaa tcacgttcta 1020
 aatcagtttg tttagataaa tcatttaata aatcatcttc agcatt 1066

<210> 13

<211> 302

<212> PRT

<213> Candida albicans

<400> 13

Met Pro Arg Phe Lys Gln Val Asp Val Phe Thr Asn Val Lys Tyr Leu
 1 5 10 15

Gly Asn Pro Val Ala Val Ile Tyr Asp Ser Asp Asn Leu Thr Thr Gln
 20 25 30

Glu Met Gln Lys Ile Ala Arg Trp Thr Asn Leu Ser Glu Thr Thr Phe

35	40	45
Ile Leu Thr Pro Lys Ser Ser Ile Ala Xaa Tyr Ser Ile Arg Ile Phe		
50	55	60
Thr Ser Gly Gly Asn Glu Leu Pro Phe Ala Gly His Pro Thr Leu Gly		
65	70	75
		80
Thr Ala Phe Ala Leu Leu Glu Asp Gly Lys Ile Lys Pro Asn Asp Asn		
85	90	95
Gly Gln Ile Ile Gln Glu Cys Gly Ala Gly Leu Val Lys Ile Ser Val		
100	105	110
Glu Lys Thr Pro Asn Asn Asn Ser Asn Glu Leu Pro Phe Leu Leu Ser		
115	120	125
Phe Glu Leu Pro Tyr Phe Lys Phe His Glu Ile Asp Asp Lys Val Ile		
130	135	140
Glu Glu Leu Gln His Ser Trp Asn Gly Thr Asn Ile Ile Gly Lys Pro		
145	150	155
		160
Val Leu Ile Asp Ala Gly Pro Lys Trp Ala Val Phe Gln Leu Gly Ser		
165	170	175
Gly Lys Glu Val Leu Asp Leu Asn Xaa Asp Leu Ala Gln Ile Glu Arg		
180	185	190
Leu Ser Leu Glu Asn Gly Trp Thr Gly Ile Gly Val Phe Gly Lys His		
195	200	205
Asn Glu Asn Gly Asp Ser Val Glu Leu Arg Asn Ile Ala Pro Ala Val		
210	215	220
Gly Val Ala Glu Asp Pro Ala Cys Gly Ser Gly Ser Gly Ala Ile Gly		
225	230	235
		240
Ala Tyr Leu Ala Asn His Val Phe Asn Glu Lys Glu Lys Phe Thr Ile		
245	250	255
Asp Ile Ser Gln Gly Lys Pro Ile Glu Arg Asp Ala Lys Ile Gln Val		
260	265	270
Lys Val Asn Arg Leu Thr Thr Lys Asn Gly Asp Leu Ser Ile His Val		
275	280	285
Gly Gly His Ala Ile Thr Cys Phe Glu Gly Thr Tyr Ser Ile		

290

295

300

<210> 14

<211> 3726

<212> DNA

<213> *Candida albicans*

<400> 14

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 attgtaaccc cctcgtatgt ttatagttat atacctgtat ataaggacta aatatatgtt 480
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gaaggcaaaa cttcagaaca aacaaataac actggtgaag aaaccaacag caaattgcgt 3060
aaattggata caaacggtaa ccacgcattt gaaagtgaat tcacaaaact attaagggaa 3120
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gttatatata gtcttcaatg tatatttaca gaatttaa atattacact gtatttgtct 3540
tttaaattgga aatcgtagaa agtatcgatg gtaatcaatt ttgtaaatta aggggaatta 3600
gggttaacaa aattacacgt cctacagatg cattgttttg tttaaggaaa aattcaaaagc 3660
taaaccacaac cagcacagac ggaagagaga aaaagaaaaa aaccaactga gatagcaaaa 3720
cctaaa
3726

```

<210> 15

<211> 942

<212> PRT

<213> Candida albicans

<400> 15

```

Met Thr Glu Thr Val Ile Glu Lys Lys Arg Lys Val Asp Leu Asn Ala
  1                      5                      10                      15

```

```

Ser Gly Ile Thr Lys Gln Pro Lys Ala Ser Lys Ile Phe Ser Pro Phe
      20                      25                      30

```

```

Arg Val Leu Gly Asn Val Thr Asp Ser Thr Pro Phe Ala Met Gly Thr
      35                      40                      45

```

```

Leu Gly Ser Thr Phe Tyr Ala Val Thr Ser Val Gly Arg Ser Phe Gln
      50                      55                      60

```

```

Ile Tyr Asp Leu Ala Thr Leu His Leu Leu Phe Val Ser Gln Thr Gln
      65                      70                      75                      80

```

```

Thr Pro Ser Arg Ile Thr Ser Leu Ala Ala His His His Tyr Val Tyr
      85                      90                      95

```

Ala Ser Tyr Gly Asp Arg Ile Gly Ile Phe Arg Arg Gly Arg Leu Glu
 100 105 110

His Glu Leu Val Cys Glu Gly Asn Ser Thr Val Asn Gln Leu Leu Val
 115 120 125

Phe Gly Glu Tyr Leu Ile Ala Thr Thr Leu Glu Gly Asp Ile Phe Val
 130 135 140

Phe Arg Lys Thr Glu Gly Lys Lys Phe Pro Thr Glu Leu Tyr Thr Thr
 145 150 155 160

Ile Arg Ile Ile Asn Ser Leu Val Glu Gly Glu Ile Val Gly Leu Ile
 165 170 175

His Pro Pro Thr Tyr Leu Asn Lys Val Ile Val Ala Thr Thr Gln Ser
 180 185 190

Val Phe Val Ile Asn Val Arg Thr Gly Lys Leu Leu Tyr Lys Ser Arg
 195 200 205

Glu Leu Gln Phe Glu Gly Glu Lys Ile Ser Ser Ile Glu Ala Ala Pro
 210 215 220

Val Leu Asp Val Ile Ala Val Gly Thr Ser Asn Gly Asn Val Phe Leu
 225 230 235 240

Phe Asn Ile Lys Lys Gly Lys Val Leu Gly Gln Lys Ile Ile Thr Ser
 245 250 255

Gly Thr Glu Ser Ser Ser Lys Val Ala Ser Ile Ser Phe Arg Thr Asp
 260 265 270

Gly Ala Pro His Leu Val Ala Gly Leu Asn Asn Gly Asp Leu Tyr Phe
 275 280 285

Tyr Asp Leu Asp Lys Lys Ser Arg Val His Val Leu Arg Asn Ala His
 290 295 300

Lys Glu Thr His Gly Gly Val Ala Asn Ala Lys Phe Leu Asn Gly Gln
 305 310 315 320

Pro Ile Val Leu Ser Asn Gly Gly Asp Asn His Leu Lys Glu Phe Val
 325 330 335

Phe Asp Pro Asn Leu Thr Thr Ser Asn Ser Ser Ile Val Pro Pro Pro
 340 345 350

Arg His Leu Arg Ser Arg Gly Gly His Ser Ala Pro Pro Val Ala Ile
 355 360 365
 Glu Phe Pro Gln Glu Asp Lys Thr His Phe Leu Leu Ser Ala Ser Arg
 370 375 380
 Asp Lys Thr Phe Trp Ile Phe Ser Leu Arg Lys Asp Ala Gln Ala Gln
 385 390 395 400
 Glu Met Ser Gln Arg Leu Gln Lys Ser Lys Asp Gly Lys Arg Gln Ala
 405 410 415
 Gly Gln Val Val Ser Met Arg Glu Lys Phe Pro Glu Ile Ile Ser Ile
 420 425 430
 Ser Ser Ser Tyr Ala Arg Glu Gly Asp Trp Glu Asn Ile Ile Thr Ala
 435 440 445
 His Lys Asp Glu Thr Phe Ala Arg Thr Trp Asp Ser Arg Asn Lys Arg
 450 455 460
 Val Gly Arg His Leu Leu Asn Thr Ile Asp Gly Gly Ile Val Lys Ser
 465 470 475 480
 Val Cys Val Ser Gln Cys Gly Asn Phe Gly Leu Val Gly Ser Ser Ser
 485 490 495
 Gly Gly Ile Gly Ser Tyr Asn Leu Gln Ser Gly Leu Leu Arg Lys Lys
 500 505 510
 Tyr Val Leu His Lys Gln Ala Val Thr Gly Leu Ala Ile Asp Gly Met
 515 520 525
 Asn Arg Lys Met Val Ser Cys Gly Leu Asp Gly Ile Val Gly Phe Tyr
 530 535 540
 Asp Phe Gly Lys Ser Val Tyr Leu Gly Lys Leu Gln Leu Glu Ala Pro
 545 550 555 560
 Ile Thr Ser Met Ile Tyr His Lys Ser Ser Asp Leu Val Ala Cys Ala
 565 570 575
 Leu Asp Asp Leu Ser Ile Val Val Ile Asp Val Thr Thr Gln Lys Val
 580 585 590
 Ile Arg Ile Leu Tyr Gly His Thr Asn Arg Ile Ser Gly Met Asp Phe
 595 600 605

Ser Pro Asp Gly Arg Trp Ile Val Ser Val Ala Leu Asp Ser Thr Leu
 610 615 620

Arg Thr Trp Asp Leu Pro Thr Gly Gly Cys Ile Asp Gly Val Ile Leu
 625 630 635 640

Pro Ile Val Ala Thr Ala Val Lys Phe Ser Pro Ile Gly Asp Ile Leu
 645 650 655

Ala Thr Thr His Val Ser Gly Asn Gly Val Ser Leu Trp Thr Asn Arg
 660 665 670

Ala Gln Phe Lys Pro Val Ser Thr Arg His Val Glu Glu Asp Glu Phe
 675 680 685

Ser Thr Ile Leu Leu Pro Asn Ala Ser Gly Asp Gly Gly Ser Thr Met
 690 695 700

Leu Asp Gly Phe Leu Asp Glu Asp Ser Asn Glu Asp Gly Thr Ile Asp
 705 710 715 720

Glu Gln Tyr Thr Ser Ala Ala Gln Ile Asp Ala Ser Leu Ile Thr Leu
 725 730 735

Ser Ser Glu Pro Arg Ser Lys Phe Asn Thr Leu Leu His Leu Asp Thr
 740 745 750

Ile Lys Gln Gln Ser Lys Pro Lys Glu Ala Pro Lys Lys Pro Glu Asn
 755 760 765

Ala Pro Phe Phe Leu Gln Leu Thr Gly Gln Ala Val Gly Asp Arg Ala
 770 775 780

Ser Val Ala Glu Gly Lys Thr Ser Glu Gln Thr Asn Asn Thr Val Glu
 785 790 795 800

Glu Thr Asn Ser Lys Leu Arg Lys Leu Asp Thr Asn Gly Asn His Ala
 805 810 815

Phe Glu Ser Glu Phe Thr Lys Leu Leu Arg Glu Ala Gly Glu Ser Gly
 820 825 830

Gln Phe Glu Arg Phe Leu Thr Tyr Leu Leu Asn Leu Ser Pro Ala Val
 835 840 845

Leu Asp Leu Glu Ile Arg Ser Leu Asn Ser Phe Val Pro Leu Thr Glu
 850 855 860

Met Thr Asn Phe Ile Gln Ala Leu Asn Ala Gly Leu Lys Ser Asn Ala
865 870 875 880

Asn Tyr Glu Ile Trp Glu Thr Leu Tyr Ala Met Phe Phe Asn Ile His
885 890 895

Gly Asp Val Ile His Gln Phe Glu Asn Glu Thr Ser Leu His Glu Ala
900 905 910

Leu Glu Glu Tyr Arg Gln Leu Asn Asp Glu Lys Asn Asn Lys Met Asp
915 920 925

Ser Leu Val Lys Tyr Cys Ala Ser Ile Val Ser Phe Ile Ser
930 935 940

<210> 16

<211> 725

<212> DNA

<213> Candida albicans

<400> 16

aacctggcaa ttaactgccc ggcaagtgat agcaggagat aggtgtgtat agattataat 60
ggaacgccga tttttgcagt atcacgcgta ataaggacag cagttggaca tcggtacatg 120
agagagcaat gtaagtcttg atagtaatga gccgtgttga agtagtattt taatctaatt 180
ttactcaaaa aaggacaatg gagatctgga gataacagca cactaatcgg ttctagacat 240
agactaagcc tgaaaggggg tactacagct tgttttgaaa aggtttgcgt tgtataggca 300
gttaaatgtg tgtttttttt gggtagaatt tgagaaaaag ttgactgaaa aaaatgcaag 360
aaacggggtg atcatgaaaa tagacacaca caaaaagtca aaaaacaatg gaaaagcttc 420
agaataagca gtaggaggtg tctgaattga gtttgtattg ttatttagag ttttaaatta 480
gagttgtaaa tttttgggta gaatttacga aaaagtcgaa caaaaaaacg acaagtcagg 540
gtgattgcaa aaaaacagaa acaatagata atcttaaatt aaggtagtag aggctctgtg 600
aagtaattta gagtttaaac aggggggcac gagtcagtgtag tagagttgtg aagtttattt 660
ggctagttaa ttgactggca agattgttaa acgtggggta gaaaaagaca acgcatcgac 720
aggtt 725

<210> 17

<211> 626

<212> DNA

<213> Candida albicans

<400> 17

attctttgtt tgtttgttga tttttgatct cttgtctaga atcactcatt aatatttgat 60
tcagggtttt gatttgctaa ataaggggtc tattaggagg atattatata taatgtgatg 120
tggcgaaaaa aaaaaacaag atctactact ctggtggatt tatttgtgat ggcgattgaa 180
gagaaaaaac gtctttttta cgcgtttttt tatttttttg agaagcaaatt ttcaagcaaa 240
gactcttatt gtgttgcttt tgatccattc aaattttgta ttacttttca ttagaactat 300

```

aactgttcat tatcaatgac gtatacatgt ctggttcctg ttatgtattg taatttttagt 360
taattataag ccgtatattg gtagtattcc tctgtactca caatggaatt ggtctttcaa 420
cagcaacaag tgttattttc cctgaatgta gaaaatgaaa ggtagtggtt acatatagtt 480
ggaaatcaag cctctgaaat gaatcacaaat ataataacaa tttgtagttg cagagaaaaa 540
caattcaagt tgacgggtag tttttttttt ttcactgcat ttttcaacga aaactaaata 600
aaatttcgct gatattgata aagtat                                     626

```

<210> 18

<211> 667

<212> DNA

<213> *Candida albicans*

<400> 18

```

tttagtttta tattgatgat gttttttaagt gcttggtttat catgggtggat ggaaattaga 60
atgagtaaat tgaatggaaa atcactgcaa caccaacaac aaccactggg ggatacgaaa 120
atttagtgta caaatctctg ccaaaaaaat acaataaaaa ccgcttatag tcttctactg 180
acataacaac acaagtcaat aaatcaacaa ctcataaaca atgtagactt aatactatcg 240
cttaattatt taaactataa taaataacct atagtattat gcctttgtca atgtgtgtag 300
aatttggtta ttacatatcc atgtgtaata tatatggtga tcaaaaaacg cgatcttctc 360
tttgggtgtag tgtgttacac aaaaaattca ctagtctagg tcacatgata atcacgtgaa 420
aatcaaaaat ttgttgaaat tgaatttcct caattttgaa attttggttg aaattttttt 480
tttgctttac aaaaagactc cattttggtt tccatttcac aaccaattac ttaattcctc 540
tttttcataa ttaataacta tcattactta caactacaaa caactacgat catttcctaa 600
gaaaaagcaa cgagggcgaa ttgagacatt aatccccttt attttatcat catgccttat 660
acagaac                                                         667

```

<210> 19

<211> 5

<212> PRT

<213> *Candida albicans*

<400> 19

Met Pro Tyr Thr Glu

1

5

<210> 20

<211> 165

<212> DNA

<213> *Candida albicans*

<400> 20

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aactattgcc aatggtaaat atgccagtga aatcgagaat ttaataagt cggtcctctc 60
taagggtcca ttcaaattca ctaatgcaca attggatctt tatgctgcta gcacacataa 120
ccaagagcca atatcctagt aacgacgcac catagtagac cgaat                                     165

```

<210> 21

<211> 564

<212> DNA

<213> *Candida albicans*

<400> 21

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aacctaaaaa tggctaagtt catcaaactct ggtaaagttg ctattgttgt aagaggctgt 60
tacgctggta aaaaagtagt cattgtgaaa ccacatgatg aaggtaccaa atctcaccca 120
ttcccacatg ccattgtcgc tggatttgaa agagctccat tgaagggttac caagaagatg 180
gatgctaaaa aagttaccaa aagaactaaa gtcaagccat ttgttaaatt agtaaactac 240
aaccatttaa tgccaactag atactcattg gatgttgaat cattcaaadc tgctgtcact 300
tctgaagctt tagaagaacc atctcaaaga gaagaagcta aaaaagttgt caagaaggct 360
tttgaagaaa aacatcaagc tggtaagaac aaatggttct tccaaaaatt acacttttaa 420
gaaaggaacc acctttattt gaatgtttgt aatatagggt gaatcagaga gacaaagtag 480
aagaaaatac aaaaaagaga gtatatctgt atagtataat ttaatggggg tctaatttac 540
ttaccacttt attcgtgcat tatt                                     564

```

<210> 22

<211> 136

<212> PRT

<213> *Candida albicans*

<400> 22

```

Met Ala Lys Phe Ile Lys Ser Gly Lys Val Ala Ile Val Val Arg Gly
  1              5              10              15

Arg Tyr Ala Gly Lys Lys Val Val Ile Val Lys Pro His Asp Glu Gly
          20              25              30

Thr Lys Ser His Pro Phe Pro His Ala Ile Val Ala Gly Ile Glu Arg
      35              40              45

Ala Pro Leu Lys Val Thr Lys Lys Met Asp Ala Lys Lys Val Thr Lys
      50              55              60

Arg Thr Lys Val Lys Pro Phe Val Lys Leu Val Asn Tyr Asn His Leu
      65              70              75              80

Met Pro Thr Arg Tyr Ser Leu Asp Val Glu Ser Phe Lys Ser Ala Val
          85              90              95

Thr Ser Glu Ala Leu Glu Glu Pro Ser Gln Arg Glu Glu Ala Lys Lys
      100              105              110

Val Val Lys Lys Ala Phe Glu Glu Lys His Gln Ala Gly Lys Asn Lys
      115              120              125

Trp Phe Phe Gln Lys Leu His Phe
      130              135

```

<210> 23

<211> 1192

<212> DNA

<213> Candida albicans

<400> 23

```

tttgaaacga ttaagtccaa tcaaacaatc ttattcaaaa gtactcgcaa tacgtacaat 60
gtcaattcca tctactcagt acggattttt ttataataaa gctagtgggc ttaatttgaa 120
aaaagacttg ccggttaaca agccagggtgc tgggtcaattg cttttaaagg ttgatgcagt 180
tggcctttgt cattcagatt tacatgttct ctatgaagggt ttggattgtg gtgataatta 240
tgtgatgggc cacgaaattg ctgggactgt tgctgaacta ggtgaagagg tgagtgaatt 300
tgcagttgga gatcgtgtcg cttgtgtcgg cccaatgga tgtggtcttt gtaaactctg 360
tcttactggg aacgataatg tttgtaccaa gtctgttttg gattgggttg gattgggtta 420
caatggagggt tacgagcaat ttttgtagt caagagacca agaaacttgg tcaagatccc 480
tgacaatggt acttccgagg aagctgcagc tattacggat gccgtattga ctctttacca 540
tgctatcaag tctgcagggtg ttggtccagc aagtaataa ttaattatcg gagctgggtg 600
attaggagggt aacgctattc aagttgcaaa agcattttgt gcgaagggtta ctgttttgga 660
taaaaaggat aaggcaagag accaagctaa ggccttttga gctgaccagg ttacagtga 720
attaccagac agcgtttttac ctgggtcatt cagtgttgtt tttgattttg tttcggttca 780
ggcaacatac gatttgtgtc aaaagtattg tgagccaaag ggtactattg ttcccgtagg 840
tctaggtgca acttcgctta acataaatct tgctgattta gatcttcgtg aaattaccgt 900
caagggctca ttctggggta ccctgatgga ttaagagaa gcatttgaat tggctgcaca 960
gggaaaggtc aaaccaaag ttgctcatgc tccattgtca gaattgccta agtatatgga 1020
gaagttgaga gccggtgggt atgaaggaag agtcgtgttt aatccataat actgaaaagt 1080
gaagaaacca tcaataatag cttggtgagt atgtatggga aatattcatt tatgtatgta 1140
ggtcatttat atgtgtgtaa tgatttctaa tctgaatttc gtacaattct tt 1192

```

<210> 24

<211> 336

<212> PRT

<213> Candida albicans

<400> 24

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Met Ser Ile Pro Ser Thr Gln Tyr Gly Phe Phe Tyr Asn Lys Ala Ser
  1                      5                      10                      15

Gly Leu Asn Leu Lys Lys Asp Leu Pro Val Asn Lys Pro Gly Ala Gly
      20                      25                      30

Gln Leu Leu Leu Lys Val Asp Ala Val Gly Leu Cys His Ser Asp Leu
      35                      40                      45

His Val Leu Tyr Glu Gly Leu Asp Cys Gly Asp Asn Tyr Val Met Gly
      50                      55                      60

His Glu Ile Ala Gly Thr Val Ala Glu Leu Gly Glu Glu Val Ser Glu
      65                      70                      75                      80

```

Phe Ala Val Gly Asp Arg Val Ala Cys Val Gly Pro Asn Gly Cys Gly
 85 90 95

Leu Cys Lys His Cys Leu Thr Gly Asn Asp Asn Val Cys Thr Lys Ser
 100 105 110

Phe Leu Asp Trp Phe Gly Leu Gly Tyr Asn Gly Gly Tyr Glu Gln Phe
 115 120 125

Leu Leu Val Lys Arg Pro Arg Asn Leu Val Lys Ile Pro Asp Asn Val
 130 135 140

Thr Ser Glu Glu Ala Ala Ala Ile Thr Asp Ala Val Leu Thr Pro Tyr
 145 150 155 160

His Ala Ile Lys Ser Ala Gly Val Gly Pro Ala Ser Asn Ile Leu Ile
 165 170 175

Ile Gly Ala Gly Gly Leu Gly Gly Asn Ala Ile Gln Val Ala Lys Ala
 180 185 190

Phe Gly Ala Lys Val Thr Val Leu Asp Lys Lys Asp Lys Ala Arg Asp
 195 200 205

Gln Ala Lys Ala Phe Gly Ala Asp Gln Val Tyr Ser Glu Leu Pro Asp
 210 215 220

Ser Val Leu Pro Gly Ser Phe Ser Ala Cys Phe Asp Phe Val Ser Val
 225 230 235 240

Gln Ala Thr Tyr Asp Leu Cys Gln Lys Tyr Cys Glu Pro Lys Gly Thr
 245 250 255

Ile Val Pro Val Gly Leu Gly Ala Thr Ser Leu Asn Ile Asn Leu Ala
 260 265 270

Asp Leu Asp Leu Arg Glu Ile Thr Val Lys Gly Ser Phe Trp Gly Thr
 275 280 285

Ser Met Asp Leu Arg Glu Ala Phe Glu Leu Ala Ala Gln Gly Lys Val
 290 295 300

Lys Pro Asn Val Ala His Ala Pro Leu Ser Glu Leu Pro Lys Tyr Met
 305 310 315 320

Glu Lys Leu Arg Ala Gly Gly Tyr Glu Gly Arg Val Val Phe Asn Pro
 325 330 335

<210> 25

<211> 2481

<212> DNA

<213> *Candida albicans*

<400> 25

```

atgactggtg aagaagataa aaaacaacat tttgatgctt ctggtgcttc tgctgtagat 60
gataaaacag caactgcaat tttaagaaga aaaaagaaag ataatgcctt ggtcggtgat 120
gacgccacca acgatgacaa ttctgtcata accatgtcgt caaacacaat ggaattgtta 180
caattattcc gtggtgatac agtcttggtg aaaggtaaga agagaaagga cacagtgttg 240
atcgttttag ctgatgatga tatgcctgat ggcgttgcta gagttaacag atgtgttcgt 300
aacaatttgc gtgtcagatt gggagatata gttactgtcc atccatgtcc tgatattaaa 360
tatgccaca gaatctcagt attgccaatt gctgatactg ttgaaggat taatgggtcc 420
ttattcgacc ttacttgaa gccatatttt gttgaagcct atagaccagt gagaaaagg 480
gatttattca ctgtgagggg tggatgaga caagtagaat tcaaagttgt tgaagttgac 540
cctgaagaaa ttgcaattgt tgctcaagat accattattc attgtgaagg agaacctatt 600
aatcgtgaag atgaagaaaa tagcttgaat gaagtgggtt acgacgatat tggagggttg 660
aagaaacaaa tggcccaaat tagagaattg gttgaattgc ctttaagaca tccacaatta 720
ttcaaatcga ttggtattaa gccaccaaag ggtattttga tgtatggtcc acctggtacc 780
ggtaaaacca ttatggcaag agcagtggcc aatgaaacag gtgccttctt tttcttaata 840
aatggtccag aaattatgtc taaaatggct ggtgagtctg aatccaattt aagaaaagct 900
tttgaagagg ctgaaaagaa ttctccttcc attattttca ttgatgagat tgactctatt 960
gccccaaaga gagacaaaac taatggtgaa gtagaaagaa gagttgtttc tcaattgtta 1020
accttatagg atggtatgaa ggccagatct aatgtagttg ttattgctgc tactaacaga 1080
ccaaattcta ttgatcctgc ttgagaaga ttggaagat tcgacagaga agttgacatt 1140
ggtgttccgg atgctgaagg acgtttagag attttgagaa tccacacaaa gaatatgaaa 1200
ttggctgatg atgttgactt ggaagccatc gcttctgaaa cacatgggtt cgttggtgct 1260
gatattgctt cattatgttc agaagctgct atgcaacaaa tccgtgaaaa gatggatctt 1320
atcgacttgg aagaagaaac cattgatact gaagtgttga actctttggg tgtcactcaa 1380
gacaacttca gatttgctct cggaaactcc aaccatctg cttgctga aactgttgtt 1440
gaaaatgtta atgtcacttg ggatgatatt ggtgggttgg acaacattaa gaatgaatta 1500
aaagaaaccg tggagtatcc tgttttacat ccagatcaat accaaaaatt cggattggca 1560
ccaacaaaag gtgttttgtt ctttgggtcca ccaggtagt gtaagacact tttggccaag 1620
gctgttgcta ctgaagtttc tgctaatttc atttctgtca aagggtccaga attgttgagt 1680
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ggtatgaatg ctaagaagaa tgtgtttgtc attggtgcca ctaacagacc agatcaaatt 1920
gatcctgcat tattgagacc aggtagattg gatcaattaa tttatgtccc attgccagat 1980
gagccagcta gattgtctat tttaacaagct caattgagaa acactccatt agaacctggg 2040
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attgttcaaa gatctgctaa atttgcatt aaagactcta ttgaagccca agtaaagatt 2160
aacaagatta aagaagaaaa agaaaagggtg aaaactgaag atgttgatat gaaggtagat 2220

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gaagttgaag aagaagaccc tgtgccttac attaccagag ctcactttga agaggctatg 2280
 aagaccgcaa aaagatctgt ttcagacgct gaattacgct gttatgagtc ttacgctcaa 2340
 caattgcaag cctcaagagg tcaattttct agcttttagat tcaatgaaaa tgctgggtgcc 2400
 actgataatg gttcagcagc aggtgccaac tcagggtgcag ctttcggaaa cgttgaagag 2460
 gaagacgatt tgtacagttg a 2481

<210> 26

<211> 826

<212> PRT

<213> Candida albicans

<400> 26

Met Thr Gly Glu Glu Asp Lys Lys Gln His Phe Asp Ala Ser Gly Ala
 1 5 10 15

Ser Ala Val Asp Asp Lys Thr Ala Thr Ala Ile Leu Arg Arg Lys Lys
 20 25 30

Lys Asp Asn Ala Leu Val Val Asp Asp Ala Thr Asn Asp Asp Asn Ser
 35 40 45

Val Ile Thr Met Ser Ser Asn Thr Met Glu Leu Leu Gln Leu Phe Arg
 50 55 60

Gly Asp Thr Val Leu Val Lys Gly Lys Lys Arg Lys Asp Thr Val Leu
 65 70 75 80

Ile Val Leu Ala Asp Asp Asp Met Pro Asp Gly Val Ala Arg Val Asn
 85 90 95

Arg Cys Val Arg Asn Asn Leu Arg Val Arg Leu Gly Asp Ile Val Thr
 100 105 110

Val His Pro Cys Pro Asp Ile Lys Tyr Ala Asn Arg Ile Ser Val Leu
 115 120 125

Pro Ile Ala Asp Thr Val Glu Gly Ile Asn Gly Ser Leu Phe Asp Leu
 130 135 140

Tyr Leu Lys Pro Tyr Phe Val Glu Ala Tyr Arg Pro Val Arg Lys Gly
 145 150 155 160

Asp Leu Phe Thr Val Arg Gly Gly Met Arg Gln Val Glu Phe Lys Val
 165 170 175

Val Glu Val Asp Pro Glu Glu Ile Ala Ile Val Ala Gln Asp Thr Ile
 180 185 190

Ile His Cys Glu Gly Glu Pro Ile Asn Arg Glu Asp Glu Glu Asn Ser
 195 200 205
 Leu Asn Glu Val Gly Tyr Asp Asp Ile Gly Gly Cys Lys Lys Gln Met
 210 215 220
 Ala Gln Ile Arg Glu Leu Val Glu Leu Pro Leu Arg His Pro Gln Leu
 225 230 235 240
 Phe Lys Ser Ile Gly Ile Lys Pro Pro Lys Gly Ile Leu Met Tyr Gly
 245 250 255
 Pro Pro Gly Thr Gly Lys Thr Ile Met Ala Arg Ala Val Ala Asn Glu
 260 265 270
 Thr Gly Ala Phe Phe Phe Leu Ile Asn Gly Pro Glu Ile Met Ser Lys
 275 280 285
 Met Ala Gly Glu Ser Glu Ser Asn Leu Arg Lys Ala Phe Glu Glu Ala
 290 295 300
 Glu Lys Asn Ser Pro Ser Ile Ile Phe Ile Asp Glu Ile Asp Ser Ile
 305 310 315 320
 Ala Pro Lys Arg Asp Lys Thr Asn Gly Glu Val Glu Arg Arg Val Val
 325 330 335
 Ser Gln Leu Leu Thr Leu Met Asp Gly Met Lys Ala Arg Ser Asn Val
 340 345 350
 Val Val Ile Ala Ala Thr Asn Arg Pro Asn Ser Ile Asp Pro Ala Leu
 355 360 365
 Arg Arg Phe Gly Arg Phe Asp Arg Glu Val Asp Ile Gly Val Pro Asp
 370 375 380
 Ala Glu Gly Arg Leu Glu Ile Leu Arg Ile His Thr Lys Asn Met Lys
 385 390 395 400
 Leu Ala Asp Asp Val Asp Leu Glu Ala Ile Ala Ser Glu Thr His Gly
 405 410 415
 Phe Val Gly Ala Asp Ile Ala Ser Leu Cys Ser Glu Ala Ala Met Gln
 420 425 430
 Gln Ile Arg Glu Lys Met Asp Leu Ile Asp Leu Glu Glu Glu Thr Ile
 435 440 445

Asp Thr Glu Val Leu Asn Ser Leu Gly Val Thr Gln Asp Asn Phe Arg
 450 455 460

Phe Ala Leu Gly Asn Ser Asn Pro Ser Ala Leu Arg Glu Thr Val Val
 465 470 475 480

Glu Asn Val Asn Val Thr Trp Asp Asp Ile Gly Gly Leu Asp Asn Ile
 485 490 495

Lys Asn Glu Leu Lys Glu Thr Val Glu Tyr Pro Val Leu His Pro Asp
 500 505 510

Gln Tyr Gln Lys Phe Gly Leu Ala Pro Thr Lys Gly Val Leu Phe Phe
 515 520 525

Gly Pro Pro Gly Thr Gly Lys Thr Leu Leu Ala Lys Ala Val Ala Thr
 530 535 540

Glu Val Ser Ala Asn Phe Ile Ser Val Lys Gly Pro Glu Leu Leu Ser
 545 550 555 560

Met Trp Tyr Gly Glu Ser Glu Ser Asn Ile Arg Asp Ile Phe Asp Lys
 565 570 575

Ala Arg Ala Ala Ala Pro Thr Val Val Phe Leu Asp Glu Leu Asp Ser
 580 585 590

Ile Ala Lys Ala Arg Gly Gly Ser His Gly Asp Ala Gly Gly Ala Ser
 595 600 605

Asp Arg Val Val Asn Gln Leu Leu Thr Glu Met Asp Gly Met Asn Ala
 610 615 620

Lys Lys Asn Val Phe Val Ile Gly Ala Thr Asn Arg Pro Asp Gln Ile
 625 630 635 640

Asp Pro Ala Leu Leu Arg Pro Gly Arg Leu Asp Gln Leu Ile Tyr Val
 645 650 655

Pro Leu Pro Asp Glu Pro Ala Arg Leu Ser Ile Leu Gln Ala Gln Leu
 660 665 670

Arg Asn Thr Pro Leu Glu Pro Gly Leu Asp Leu Asn Glu Ile Ala Lys
 675 680 685

Ile Thr His Gly Phe Ser Gly Ala Asp Leu Ser Tyr Ile Val Gln Arg
 690 695 700

Ser Ala Lys Phe Ala Ile Lys Asp Ser Ile Glu Ala Gln Val Lys Ile
 705 710 715 720

Asn Lys Ile Lys Glu Glu Lys Glu Lys Val Lys Thr Glu Asp Val Asp
 725 730 735

Met Lys Val Asp Glu Val Glu Glu Glu Asp Pro Val Pro Tyr Ile Thr
 740 745 750

Arg Ala His Phe Glu Glu Ala Met Lys Thr Ala Lys Arg Ser Val Ser
 755 760 765

Asp Ala Glu Leu Arg Arg Tyr Glu Ser Tyr Ala Gln Gln Leu Gln Ala
 770 775 780

Ser Arg Gly Gln Phe Ser Ser Phe Arg Phe Asn Glu Asn Ala Gly Ala
 785 790 795 800

Thr Asp Asn Gly Ser Ala Ala Gly Ala Asn Ser Gly Ala Ala Phe Gly
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Asn Val Glu Glu Glu Asp Asp Leu Tyr Ser
 820 825

<210> 27

<211> 1918

<212> DNA

<213> Candida albicans

<400> 27

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<210> 28

<211> 466

<212> PRT

<213> *Candida albicans*

<400> 28

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Lys Gln Arg Leu Glu Glu Ile Leu Pro Ala Lys Ala Glu Glu Val Lys
 35 40 45

Gln Phe Lys Lys Glu His Gly Lys Thr Val Ile Gly Glu Val Leu Leu
 50 55 60

Glu Gln Ala Tyr Gly Gly Met Arg Gly Ile Lys Gly Leu Val Trp Glu
 65 70 75 80

Gly Ser Val Leu Asp Pro Ile Glu Gly Ile Arg Phe Arg Gly Arg Thr
 85 90 95

Ile Pro Asp Ile Gln Lys Glu Leu Pro Lys Ala Pro Gly Gly Glu Glu
 100 105 110

Pro Leu Pro Glu Ala Leu Phe Trp Leu Leu Leu Thr Gly Glu Val Pro
 115 120 125

Thr Asp Ala Gln Thr Lys Ala Leu Ser Glu Glu Phe Ala Ala Arg Ser
 130 135 140

Ala Leu Pro Lys His Val Glu Glu Leu Ile Asp Arg Ser Pro Ser His
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 Leu His Pro Met Ala Gln Phe Ser Ile Ala Val Thr Ala Leu Glu Ser
 165 170 175
 Glu Ser Gln Phe Ala Gln Ala Tyr Ala Lys Gly Ala Asn Lys Ser Glu
 180 185 190
 Tyr Trp Lys Tyr Thr Tyr Glu Asp Ser Ile Asp Leu Leu Ala Lys Leu
 195 200 205
 Pro Thr Ile Ala Ala Lys Ile Tyr Arg Asn Val Phe His Asp Gly Lys
 210 215 220
 Leu Pro Ala Ala Ile Asp Ser Lys Leu Asp Tyr Gly Ala Asn Leu Ala
 225 230 235 240
 Ser Leu Leu Gly Phe Gly Asp Asn Lys Glu Phe Val Glu Leu Met Arg
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 Leu Tyr Leu Thr Ile His Ser Asp His Glu Gly Gly Asn Val Ser Ala
 260 265 270
 His Thr Thr His Leu Val Gly Ser Ala Leu Ser Ser Pro Phe Leu Ser
 275 280 285
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 Asn Gln Glu Val Leu Glu Trp Leu Phe Lys Leu Arg Glu Glu Leu Asn
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 Gly Asp Tyr Ser Lys Glu Ala Ile Glu Lys Tyr Leu Trp Glu Thr Leu
 325 330 335
 Asn Ser Gly Arg Val Val Pro Gly Tyr Gly His Ala Val Leu Arg Lys
 340 345 350
 Thr Asp Pro Arg Tyr Thr Ala Gln Arg Glu Phe Ala Leu Lys His Met
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 Pro Asp Tyr Glu Leu Phe Lys Leu Val Ser Asn Ile Tyr Glu Val Ala
 370 375 380
 Pro Gly Val Leu Thr Lys His Gly Lys Thr Lys Asn Pro Trp Pro Asn
 385 390 395 400

Val Asp Ser His Ser Gly Val Leu Leu Gln Tyr Tyr Gly Leu Thr Glu
 405 410 415

Gln Ser Phe Tyr Thr Val Leu Phe Gly Val Ser Arg Ala Phe Gly Val
 420 425 430

Leu Pro Gln Leu Ile Leu Asp Arg Gly Ile Gly Met Pro Ile Glu Arg
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Pro Lys Ser Phe Ser Thr Glu Lys Tyr Ile Glu Leu Val Lys Asn Ile
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Asn Lys
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<210> 29

<211> 2862

<212> DNA

<213> Candida albicans

<400> 29

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<210> 30

<211> 953

<212> PRT

<213> *Candida albicans*

<400> 30

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Ile Lys Asp Glu Gln Phe Glu Asn Phe Leu Lys Phe Glu Tyr Cys Arg
      20             25             30

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Ala Leu Leu Ser Gln Thr Asn Asn Asn Pro Thr Asn Asp Val Lys Phe
 35             40             45

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Ser Gln Ile Phe Leu Asp Leu Lys Lys Arg Ser Gln Asn Trp Lys Ser
 50             55             60

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Phe Asp Asp Ile Ile Gln Leu Ser Leu Leu Gln Leu Gln Tyr Cys Ile
 65             70             75             80

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Tyr Ala Lys Asn Ser Ile Lys Ala Lys Asp Arg Phe Asn Gly Ile Leu
      85             90             95

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Gln Thr Leu Leu Lys Lys Pro Gln Phe Asn Ile Ser Lys Ser Lys Asn
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Leu Pro Ile Val Ser Lys Leu Gln Asn Phe Leu Ile Leu Gly Lys Phe
 115 120 125

Gln Leu Leu Ala Cys His Val Asn Asn His Ile Ile His Asn Lys Ile
 130 135 140

Glu Ala Phe Asn Asn Ile Lys Thr Gly Ile Gln Leu Leu Tyr Ser Ile
 145 150 155 160

Val Lys Lys Leu Pro Thr Asn Ile Asn Lys Thr Leu Trp Gln Glu Leu
 165 170 175

Asn Trp Glu Ile Thr Arg Leu Leu Phe Asp Ser Tyr Lys Leu Ala Ile
 180 185 190

Asp Leu Ser Ile Asp Ile Gly Ile Ser Arg Asp Ile Pro Leu Phe Leu
 195 200 205

Asn Glu Trp Val Lys Leu Asn Asn Ser Ile Asp Asn Asp Val Pro Ile
 210 215 220

Val Asn Cys Ile Asn Glu Phe Glu Ile Gly Arg Tyr Gly Leu Leu Ser
 225 230 235 240

Asn Asn Glu Phe Gln Lys Tyr Ile Arg Ile Ala Gln Gly Arg Leu Gly
 245 250 255

Tyr Ser Leu Val Lys Asn Asn Ser Ala Val Gln Gln Tyr Ile Asn Arg
 260 265 270

Asp Arg Asp Asp Glu Ile Cys Gly His Ala Ser Ser Ser Arg Gln Leu
 275 280 285

Lys Ser Leu Val Arg Thr Ile Phe Asn Ser Asp Asn Ser Leu Ser Glu
 290 295 300

Leu Ser Lys Ser Val Gln Leu Leu Pro Cys Ile Ile Gly Asp Ser Ser
 305 310 315 320

Thr Met Cys Ser Lys Glu Leu Leu Asp Lys Leu Val Gln Leu Lys Asn
 325 330 335

Glu Ile Leu Thr Glu Val Thr Asn Tyr Glu Lys Ser Ser Ser Leu Ser
 340 345 350

Leu Asn Gln Gln Gln Gln Leu Ile Asn Asn Leu Asn Gln Val Val Cys
 355 360 365

Leu Leu Ser Ser Leu Thr Ser Phe Lys Gly Asp Gly Leu Leu Ser Glu
 370 375 380

Val Tyr Tyr Leu Gln Asp Tyr Val Arg Asn Leu Pro Phe Ala Asn Glu
 385 390 395 400

Arg Lys Leu Met Asp Ser Ser Lys Gln Asp Glu Ser Asn Asn Leu Leu
 405 410 415

Pro Arg Ala Leu Asp Phe Asn Gln Val Val Glu Asp Pro Ser Asn Thr
 420 425 430

Thr Ile Asn Asn Ser Met Ile Asp Phe Asn Val Asp Leu Gln Leu Tyr
 435 440 445

Leu Pro His Asn Trp Ile Leu Val Thr Leu Asp Ile Cys Gln Asn Thr
 450 455 460

Gly Asp Leu Leu Ile Ser Lys Leu Thr Lys Gly Ser Pro Asn Pro Ile
 465 470 475 480

Phe Met Arg Leu Pro Leu Ser Arg Phe Pro Ser Ser Leu Gly Phe Gln
 485 490 495

Gln Leu Met Gln Asn Phe Glu Lys Ile Ile Asp Asp Ser Asn Leu Ser
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Thr Lys Arg Lys Thr Thr Ser Lys Ile Leu Thr Val Glu Asp Arg Lys
 515 520 525

Gln Trp Trp Arg Ser Arg Phe Thr Leu Asp Phe Gln Leu Gln Asp Ile
 530 535 540

Leu His His Val Glu Ser Lys Trp Phe Gly Gly Phe Ile Ser Gly Ile
 545 550 555 560

Phe Thr Asn Asp Asn Asp Val Glu Asn Glu Ser Lys Asn Val Phe His
 565 570 575

Lys Phe Lys Gln Asp Leu Met Lys Ile Leu Lys Asp Cys Leu Thr Val
 580 585 590

Ser Asp Asp Lys Ser Asn Ile Glu Arg Phe Leu Gln Phe Asn Glu Phe
 595 600 605

Ile Tyr Tyr Cys Phe Tyr Ser Met Glu Glu Tyr Asn Tyr Glu Leu Val
 610 615 620

Asp Asp Leu Ile Lys Phe Ile Thr Ile Asn Met Asn Ser His Gly Arg
 625 630 635 640

Ile Val Asn Phe Gly Thr Asn Val Lys Ile Asn Lys Leu His Glu Leu
 645 650 655

Ile Lys Asn Leu Ile Asp Lys Val Asn Lys Asn Lys Gln Asn Val Thr
 660 665 670

Ser Asn Asn Lys Asn Asn Ser Asn Asn Asn Ser Asn Asn Asn Ser Asn
 675 680 685

Ser Asn Asn Ser Gln His Ile Val Leu Ile Pro Asn Ala Asn Cys Ser
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Asn Phe Pro Trp Glu Ser Met Glu Phe Leu Arg Ser Lys Ser Ile Ser
 705 710 715 720

Arg Met Pro Ser Ile His Met Leu Leu Asp Leu Val Lys Ser Asn Thr
 725 730 735

Asn Asn Lys Asn Lys Leu Met Phe Val Asp Lys Ser Asn Leu Tyr Tyr
 740 745 750

Leu Ile Asn Pro Ser Gly Asp Leu Ile Arg Ser Glu Asn Arg Phe Lys
 755 760 765

Lys Leu Phe Glu Ser Asn His Leu Trp Arg Gly Glu Ile Gly Lys Leu
 770 775 780

Ser Ser Asn Glu His Glu Asp Tyr Gln Asp Ser Ile Leu Cys Glu Ile
 785 790 795 800

Leu Lys Ser His Leu Phe Val Tyr Ile Gly His Gly Gly Cys Asp Gln
 805 810 815

Tyr Ile Lys Val Ser Lys Leu Phe Lys Lys Cys Gly Asn Asn Gln Asp
 820 825 830

Leu Ser Asn Lys Leu Pro Pro Ser Leu Leu Leu Gly Cys Ser Ser Val
 835 840 845

Lys Leu Asp Asn Cys Asn Tyr Asn Tyr Asn Ser Ser Met Leu Gln Pro
 850 855 860

Ser Gly Asn Ile Tyr Asn Trp Leu Asn Cys Lys Ser Ser Met Ile Leu
 865 870 875 880

Gly Asn Leu Trp Asp Val Thr Asp Lys Asp Ile Asp Ile Phe Thr Leu
 885 890 895

Ser Leu Leu Gln Lys Trp Gly Leu Ile Asp Asp Tyr Asn Gly Ser Gly
 900 905 910

His Asp Tyr Gly Met Lys Lys Leu Asp Leu Thr Asn Cys Val Val Gln
 915 920 925

Ser Arg Ser Lys Cys Thr Leu Lys Tyr Leu Asn Gly Ser Ala Pro Val
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Val Tyr Gly Leu Pro Met Tyr Leu Lys
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<210> 31

<211> 1443

<212> DNA

<213> Candida albicans

<400> 31

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<210> 32

<211> 399

<212> PRT

<213> Candida albicans

<400> 32

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Leu Lys Pro Asp Leu Leu Lys Gly Ile Tyr Ala Tyr Gly Phe Glu Ala
 35 40 45

Pro Ser Ala Ile Gln Ser Arg Ala Ile Met Gln Ile Ile Ser Gly Arg
 50 55 60

Asp Thr Ile Ala Gln Ala Gln Ser Gly Thr Gly Lys Thr Ala Thr Phe
 65 70 75 80

Ser Ile Gly Met Leu Glu Val Ile Asp Thr Lys Ser Lys Glu Cys Gln
 85 90 95

Ala Leu Ile Leu Ser Pro Thr Arg Glu Leu Ala Ile Gln Ile Gln Asn
 100 105 110

Val Val Met His Leu Gly Asp Tyr Met Asn Ile His Thr His Ala Cys
 115 120 125

Ile Gly Gly Lys Asn Val Gly Glu Asp Val Lys Lys Leu Gln Gln Gly
 130 135 140

Gln Gln Ile Val Ser Gly Thr Pro Gly Arg Val Ile Asp Val Ile Lys
 145 150 155 160

Arg Arg Asn Leu Gln Thr Arg Asn Ile Lys Val Leu Ile Leu Asp Glu
 165 170 175

Ala Asp Glu Leu Phe Thr Lys Gly Phe Lys Glu Gln Ile Tyr Glu Ile
 180 185 190

Tyr Lys His Leu Pro Pro Ser Val Gln Val Val Val Val Ser Ala Thr
 195 200 205

Leu Pro Arg Glu Val Leu Glu Met Thr Ser Lys Phe Thr Thr Asp Pro
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 Val Lys Ile Leu Val Lys Arg Asp Glu Ile Ser Leu Ser Gly Ile Lys
 225 230 235 240
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 245 250 255
 Cys Asp Leu Tyr Asp Asn Leu Thr Ile Thr Gln Ala Val Ile Phe Cys
 260 265 270
 Asn Thr Lys Leu Lys Val Asn Trp Leu Ala Asp Gln Met Lys Lys Gln
 275 280 285
 Asn Phe Thr Val Val Ala Met His Gly Asp Met Lys Gln Asp Glu Arg
 290 295 300
 Asp Ser Ile Met Asn Asp Phe Arg Arg Gly Asn Ser Arg Val Leu Ile
 305 310 315 320
 Ser Thr Asp Val Trp Ala Arg Gly Ile Asp Val Gln Gln Val Ser Leu
 325 330 335
 Val Ile Asn Tyr Asp Leu Pro Thr Asp Lys Glu Asn Tyr Ile His Arg
 340 345 350
 Ile Gly Arg Ser Gly Arg Phe Gly Arg Lys Gly Thr Ala Ile Asn Leu
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 Ser Thr Lys Ile Lys Glu Met Pro Met Asn Ile Asn Asp Ile Met
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 <211> 825
 <212> DNA
 <213> Candida albicans

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<210> 34

<211> 206

<212> PRT

<213> Candida albicans

<400> 34

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Met Ile Ser Gly Met Leu Tyr Asn Cys Leu Gln Lys Glu Leu Glu Thr
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Thr Arg Met Ser Cys Arg Asp Tyr Met Leu Asp Tyr Gly Ser Phe Arg
          20             25             30

Thr Arg Asp Tyr Lys Thr Thr Gln Glu Phe Leu Asp Ala Lys Tyr Lys
  35             40             45

His Leu Glu Ser Phe Ile Gly His Val Gly Lys Asn Ala Phe Met Glu
  50             55             60

Tyr Pro Ile Tyr Phe Asp Tyr Gly Phe Asn Thr Tyr Leu Gly Asp Asn
  65             70             75             80

Phe Tyr Ser Asn Tyr Asn Leu Thr Ile Leu Asp Val Ser Ile Val Arg
          85             90             95

Ile Gly Asn Asn Val Lys Cys Gly Pro Asn Val Ser Ile Leu Thr Pro
 100             105             110

Thr His Pro Val Asp Pro Thr Leu Arg Tyr Asp Gln Leu Glu Asn Ala
 115             120             125

Leu Pro Val Thr Val Gly Asn Gly Val Trp Leu Cys Gly Ser Cys Thr
 130             135             140

Ile Leu Gly Gly Val Thr Val Gly Asp Gly Ser Ile Val Ala Ala Gly
 145             150             155             160

Ala Val Val Asn Lys Asp Val Pro Pro Asn Thr Val Val Ala Gly Val
 165             170             175

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Pro Ala Arg Val Val Lys Gln Leu Glu Pro Arg Asp Pro Asn Phe Asp
 180 185 190

Thr Met Ala Val Leu Lys Gln Tyr Gly Met Gly Tyr Ile Asp
 195 200 205

<210> 35

<211> 823

<212> DNA

<213> Candida albicans

<400> 35

aaccaacaat gagtcaagtc gctccaaagt ggtaccaatc agaagacgtt ccagctccaa 60
 aacaaaccag aaagactgct cgtccacaaa aattacgtgc ctcttttagtc ccagggtaccg 120
 ttttaatttt attggccggt agattcagag gtaaaagagt tgtttacttg aagaacttgg 180
 aagacaacac cttattgggt tctgggtccat tcaaagtcaa tgggtgttcca ttgagaagag 240
 ttaacgctag atacgttatc gccacctcca ccaaagtcaa cgtttctggt gttgatgttt 300
 ctaaattcaa cgtcgaatac ttgctagag aaaaatcttc taaatctaaa aaatccgaag 360
 ctgaattctt caatgaatct caaccaaaga aagaaatcaa agctgaaaga gttgctgacc 420
 aaaaatctgt cgatgctgct ttattaagtg aaatcaaaaa gaccccataa ttgaaacaat 480
 acttggccgc ttcattctct ttgaagaacg gtgacagacc acacttggtt aaattttaat 540
 ttaggtgaaa ttaatatattt gcaaacatgt tcatgataaa taacaatgtg gctttttaag 600
 caatggatgg gatattggtt agaggatgtc tttatatattt gagttttata tatgggtact 660
 ttgtttaata atggaaggta ttggctcaga tgaacttcaa aatggagatt acttttttct 720
 tttactttta caatatattt gtctatttgc tgtttaagct gcaaaaacaa atttttaatc 780
 ggtgtatctt aactcttatt cattttgtat atttaataca tat 823

<210> 36

<211> 176

<212> PRT

<213> Candida albicans

<400> 36

Met Ser Gln Val Ala Pro Lys Trp Tyr Gln Ser Glu Asp Val Pro Ala
 1 5 10 15

Pro Lys Gln Thr Arg Lys Thr Ala Arg Pro Gln Lys Leu Arg Ala Ser
 20 25 30

Leu Val Pro Gly Thr Val Leu Ile Leu Leu Ala Gly Arg Phe Arg Gly
 35 40 45

Lys Arg Val Val Tyr Leu Lys Asn Leu Glu Asp Asn Thr Leu Leu Val
 50 55 60

Ser Gly Pro Phe Lys Val Asn Gly Val Pro Leu Arg Arg Val Asn Ala

65					70						75					80
Arg	Tyr	Val	Ile	Ala	Thr	Ser	Thr	Lys	Val	Asn	Val	Ser	Gly	Val	Asp	
				85					90					95		
Val	Ser	Lys	Phe	Asn	Val	Glu	Tyr	Phe	Ala	Arg	Glu	Lys	Ser	Ser	Lys	
			100					105					110			
Ser	Lys	Lys	Ser	Glu	Ala	Glu	Phe	Phe	Asn	Glu	Ser	Gln	Pro	Lys	Lys	
		115					120					125				
Glu	Ile	Lys	Ala	Glu	Arg	Val	Ala	Asp	Gln	Lys	Ser	Val	Asp	Ala	Ala	
	130					135					140					
Leu	Leu	Ser	Glu	Ile	Lys	Lys	Thr	Pro	Leu	Leu	Lys	Gln	Tyr	Leu	Ala	
145					150					155					160	
Ala	Ser	Phe	Ser	Leu	Lys	Asn	Gly	Asp	Arg	Pro	His	Leu	Leu	Lys	Phe	
				165					170					175		

<210> 37

<211> 415

<212> DNA

<213> Candida albicans

<400> 37

aacattaaag	caagatggaa	aacgataaag	gtcaattagt	tgaattatac	gtcccaagaa	60
aatgttctgc	taccaacaga	atcattaaag	caaagatca	cgcttctgtt	caaatctcaa	120
ttgctaaaag	tgatgaagac	ggtagagcta	ttgctggtga	aaacatcact	tacgctttaa	180
gtggttacgt	tagaggtaga	ggtgaaactg	atgactcatt	aaacagattg	gctcaacaag	240
acggtttatt	gaagaacgtc	tgggtcttact	ctcgттаага	gaatagaaga	atagacaaaa	300
ttgataattg	ggatttttaa	gaaattactt	tttttatatt	gcaaattaat	tttaatcttt	360
cttctgtgta	tatttaatgt	cttaacataa	taaaaaaaaa	gaatagaaat	ggttt	415

<210> 38

<211> 87

<212> PRT

<213> Candida albicans

<400> 38

Met Glu Asn Asp Lys Gly Gln Leu Val Glu Leu Tyr Val Pro Arg Lys
1 5 10 15

Cys Ser Ala Thr Asn Arg Ile Ile Lys Ala Lys Asp His Ala Ser Val

20 25 30
 Gln Ile Ser Ile Ala Lys Val Asp Glu Asp Gly Arg Ala Ile Ala Gly
 35 40 45
 Glu Asn Ile Thr Tyr Ala Leu Ser Gly Tyr Val Arg Gly Arg Gly Glu
 50 55 60
 Ala Asp Asp Ser Leu Asn Arg Leu Ala Gln Gln Asp Gly Leu Leu Lys
 65 70 75 80
 Asn Val Trp Ser Tyr Ser Arg
 85

<210> 39
 <211> 1685
 <212> DNA
 <213> Candida albicans

<400> 39
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 tggtagcttat ggtttgattt accttgtgga aaatatctac actaaacaac aatttgctgc 120
 taaaatgggtt cttgaacagc cattactcaa acaaaagcaa caacaacaac aaagtcacat 180
 tggacataaaa ggagaatcta gtatgaacaa acaataata ctgcaagaat tttatcaata 240
 tttttttaaac aatagtatgc cacaaccacg aaatttggac ttgaattacc ttcgagacaa 300
 cggacatgat tgcccccttt tgactgaaat ctcattacat ttaaaagtac atcaacaccc 360
 aaacatagcg actattcatc aagtattaaa cattgaagat tttgccataa taatattgat 420
 ggatcatttt gagcaaggag atttgttcac taatatcatt gatagacaaa tattcaccaa 480
 taatagtcac agaaaagttc caagaacaga ttttgaaacc caattattaa tgaagaatgc 540
 catgtttacaa ttgatagaag ccattgaata ttgtcacgaa aataatattt accattgtga 600
 tttaaaacca gaaaacatta tgggttagata taatccatac tatgttcgtc caactatcaa 660
 taacaataat aacaatggag aagatgattt atgctatgcc aacagtatta ttgactataa 720
 tgaattacac ctctgtgttg ttgattttgg tttagctatg gactctgcta ccatttgttg 780
 taattcatgt cgtggatcgt cattttacat ggcaccagaa agaaccacca attataacac 840
 ccatcgttta atcaaccaat taattgatat gaatcaatat gagtcaattg aaatcaatgg 900
 gacaacagtg acaaatcaa actgtaaata tttacctaca ttggctgggg atatttgggtc 960
 attgggagta ttgttcatta atatcacttg ttcaagaaac ccatggccca ttgcatcatt 1020
 tgataataat caaaataatg aagtgtttta gaattatatg ttgaataata acaaggctgt 1080
 tttgagcaaa atcttaccac tttcctcaca atttaatcgc ttattagata gaattttcaa 1140
 attgaatcct aatgatagaa tagatttacc aactttatac aaagaagtta ttcgttgtga 1200
 tttcttcaaa gatgatcatt actactatgc ccaacatcaa catcatcaca atcacaatca 1260
 aatcaataat gcttacaatc actatcagaa acaacctaat caagcaagac ctactgcaaa 1320
 ccaacaattg tatacaccac cggaaaccac cacttataat tcatacgcta gtgatatgga 1380
 agaagatgaa attagtgatg atgagtttta ttctgatgaa gaagatgaag atattgaaga 1440
 ctatgaagag gaagaggaag agtatttttg taatgagcaa caacaacaac agcaagtcac 1500
 aacagtgaat ggtaattttg gtcaagttaa aggtacctgt tattacgata ccaaaaccaa 1560
 aacaactaca tatataaaac caccagctgc atatacttta gagacgcta gtcaaagtgt 1620

tgaataactgt taagttgtac acataaataa ttaatgacaa ttaataataa cgattaataa 1680
tatag 1685

<210> 40

<211> 537

<212> PRT

<213> Candida albicans

<400> 40

Met Leu Asn His Glu Leu Arg Phe Ile Arg Lys Ile Gly Ala Gly Thr
1 5 10 15

Tyr Gly Leu Ile Tyr Leu Val Glu Asn Ile Tyr Thr Lys Gln Gln Phe
20 25 30

Ala Ala Lys Met Val Leu Glu Gln Pro Leu Leu Lys Gln Lys Gln Gln
35 40 45

Gln Gln Gln Ser His His Gly His Lys Gly Glu Ser Ser Met Asn Lys
50 55 60

Gln Ile Ile Ser Gln Glu Phe Tyr Gln Tyr Phe Leu Asn Asn Ser Met
65 70 75 80

Pro Gln Pro Arg Asn Leu Asp Leu Asn Tyr Leu Arg Asp Asn Gly His
85 90 95

Asp Cys Pro Phe Leu Thr Glu Ile Ser Leu His Leu Lys Val His Gln
100 105 110

His Pro Asn Ile Ala Thr Ile His Gln Val Leu Asn Ile Glu Asp Phe
115 120 125

Ala Ile Ile Ile Leu Met Asp His Phe Glu Gln Gly Asp Leu Phe Thr
130 135 140

Asn Ile Ile Asp Arg Gln Ile Phe Thr Asn Asn Ser His Arg Lys Val
145 150 155 160

Pro Arg Thr Asp Phe Glu Thr Gln Leu Leu Met Lys Asn Ala Met Leu
165 170 175

Gln Leu Ile Glu Ala Ile Glu Tyr Cys His Glu Asn Asn Ile Tyr His
180 185 190

Cys Asp Leu Lys Pro Glu Asn Ile Met Val Arg Tyr Asn Pro Tyr Tyr
195 200 205

Val Arg Pro Thr Ile Asn Asn Asn Asn Asn Asn Gly Glu Asp Asp Leu
 210 215 220

Cys Tyr Ala Asn Ser Ile Ile Asp Tyr Asn Glu Leu His Leu Val Leu
 225 230 235 240

Ile Asp Phe Gly Leu Ala Met Asp Ser Ala Thr Ile Cys Cys Asn Ser
 245 250 255

Cys Arg Gly Ser Ser Phe Tyr Met Ala Pro Glu Arg Thr Thr Asn Tyr
 260 265 270

Asn Thr His Arg Leu Ile Asn Gln Leu Ile Asp Met Asn Gln Tyr Glu
 275 280 285

Ser Ile Glu Ile Asn Gly Thr Thr Val Thr Lys Ser Asn Cys Lys Tyr
 290 295 300

Leu Pro Thr Leu Ala Gly Asp Ile Trp Ser Leu Gly Val Leu Phe Ile
 305 310 315 320

Asn Ile Thr Cys Ser Arg Asn Pro Trp Pro Ile Ala Ser Phe Asp Asn
 325 330 335

Asn Gln Asn Asn Glu Val Phe Lys Asn Tyr Met Leu Asn Asn Asn Lys
 340 345 350

Ala Val Leu Ser Lys Ile Leu Pro Ile Ser Ser Gln Phe Asn Arg Leu
 355 360 365

Leu Asp Arg Ile Phe Lys Leu Asn Pro Asn Asp Arg Ile Asp Leu Pro
 370 375 380

Thr Leu Tyr Lys Glu Val Ile Arg Cys Asp Phe Phe Lys Asp Asp His
 385 390 395 400

Tyr Tyr Tyr Ala Gln His Gln His His His Asn His Asn Gln Ile Asn
 405 410 415

Asn Ala Tyr Asn His Tyr Gln Lys Gln Pro Asn Gln Ala Arg Pro Thr
 420 425 430

Ala Asn Gln Gln Leu Tyr Thr Pro Pro Glu Thr Thr Thr Tyr Asn Ser
 435 440 445

Tyr Ala Ser Asp Met Glu Glu Asp Glu Ile Ser Asp Asp Glu Phe Tyr
 450 455 460

Ser Asp Glu Glu Asp Glu Asp Ile Glu Asp Tyr Glu Glu Glu Glu Glu
 465 470 475 480

Glu Tyr Phe Gly Asn Glu Gln Gln Gln Gln Gln Val Thr Thr Val
 485 490 495

Asn Gly Asn Phe Gly Gln Val Lys Gly Thr Cys Tyr Tyr Asp Thr Lys
 500 505 510

Thr Lys Thr Thr Thr Tyr Ile Lys Pro Pro Ala Ala Tyr Thr Leu Glu
 515 520 525

Thr Pro Ser Gln Ser Val Glu Tyr Cys
 530 535

<210> 41

<211> 848

<212> DNA

<213> Candida albicans

<400> 41

aaccaatttt agaaacaatg gtcgtcaat ttttcgtagg tggtaacttc aaagctaacg 60
 gtaccaaaca acaaatcact tcaatcatcg acaacttgaa caaggctgat ttaccaaagg 120
 atgtcgaagt tgtcatttgt ccacccgccc tttaccttgg tttagctgta gagcaaaaca 180
 aacaaccaac tgttgccatt ggtgctcaaa atgtttttga caagtcatgt ggtgctttca 240
 ctggtgaaac ctgtgcttct caaatcttgg atgttggtgc cagctggact ttaactgggc 300
 acagtgaaag aagaaccatt atcaaagaat ccgatgaatt cattgctgaa aaaaccaagt 360
 ttgccttgga cactggtgtc aaagttattt tatgtattgg tgaaacctta gaggaagaa 420
 aaggtggtgt cactttggat gtttgtgcca gacaattgga tgctgtttcc aagattgttt 480
 ctgattggtc aaacattggt gttgcttacg aacctgtttg ggcaattggg actggttttag 540
 ccgctacccc agaagatgct gaagaaaccc acaaaggat tagagctcat ttggccaaga 600
 ccattggtgc cgaacaagct gaaaaaacca gaatcttgta cgggtggttca gttaacggta 660
 agaacgctaa ggatttcaaa gacaaagcaa atgttgatgg tttcttagtc ggtggtgctt 720
 cattaataacc agaatttgtt gatatcatca aatctagatt ataaacagta tattaataaac 780
 tatatgccta tagaatttag catgttggtg tgaatttgta atgaatctat aaaaatgtgc 840
 tcatgaac 848

<210> 42

<211> 248

<212> PRT

<213> Candida albicans

<400> 42

Met Ala Arg Gln Phe Phe Val Gly Gly Asn Phe Lys Ala Asn Gly Thr
 1 5 10 15

Lys Gln Gln Ile Thr Ser Ile Ile Asp Asn Leu Asn Lys Ala Asp Leu

20	25	30
Pro Lys Asp Val Glu Val Val Ile Cys Pro Pro Ala Leu Tyr Leu Gly		
35	40	45
Leu Ala Val Glu Gln Asn Lys Gln Pro Thr Val Ala Ile Gly Ala Gln		
50	55	60
Asn Val Phe Asp Lys Ser Cys Gly Ala Phe Thr Gly Glu Thr Cys Ala		
65	70	75 80
Ser Gln Ile Leu Asp Val Gly Ala Ser Trp Thr Leu Thr Gly His Ser		
85	90	95
Glu Arg Arg Thr Ile Ile Lys Glu Ser Asp Glu Phe Ile Ala Glu Lys		
100	105	110
Thr Lys Phe Ala Leu Asp Thr Gly Val Lys Val Ile Leu Cys Ile Gly		
115	120	125
Glu Thr Leu Glu Glu Arg Lys Gly Gly Val Thr Leu Asp Val Cys Ala		
130	135	140
Arg Gln Leu Asp Ala Val Ser Lys Ile Val Ser Asp Trp Ser Asn Ile		
145	150	155 160
Val Val Ala Tyr Glu Pro Val Trp Ala Ile Gly Thr Gly Leu Ala Ala		
165	170	175
Thr Pro Glu Asp Ala Glu Glu Thr His Lys Gly Ile Arg Ala His Leu		
180	185	190
Ala Lys Thr Ile Gly Ala Glu Gln Ala Glu Lys Thr Arg Ile Leu Tyr		
195	200	205
Gly Gly Ser Val Asn Gly Lys Asn Ala Lys Asp Phe Lys Asp Lys Ala		
210	215	220
Asn Val Asp Gly Phe Leu Val Gly Gly Ala Ser Leu Lys Pro Glu Phe		
225	230	235 240
Val Asp Ile Ile Lys Ser Arg Leu		
245		

<210> 43
 <211> 550
 <212> PRT

<213> *Candida albicans*

<400> 43

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Met Ser Leu Asp Asn Ser Thr Glu Asn Arg Asp Leu Glu Glu Lys Glu
  1              5              10              15

Glu Ile Pro Lys Asn Glu His Asn Glu Gln Gly Glu Gln Asn Glu Asn
      20              25              30

Asn Glu His Ile Pro Thr Leu Glu Asp Lys Pro Leu Lys Glu Tyr Ile
      35              40              45

Gly Ile Ser Ile Leu Cys Phe Leu Ile Ala Phe Gly Gly Phe Val Phe
      50              55              60

Gly Phe Asp Thr Gly Thr Ile Ser Gly Phe Ile Asn Met Thr Asp Phe
      65              70              75              80

Leu Glu Arg Phe Gly Gly Thr Lys Ala Asp Gly Thr Leu Tyr Phe Ser
      85              90              95

Asn Val Arg Thr Gly Leu Leu Ile Gly Leu Phe Asn Val Gly Cys Ala
      100             105             110

Ile Gly Ala Leu Phe Leu Ser Lys Val Gly Asp Met Tyr Gly Arg Arg
      115             120             125

Val Gly Ile Met Thr Ala Met Ile Ile Tyr Ile Val Gly Ile Ile Val
      130             135             140

Gln Ile Ala Ser Gln His Ala Trp Tyr Gln Ile Met Ile Gly Arg Ile
      145             150             155             160

Ile Thr Gly Leu Ala Val Gly Met Leu Ser Val Leu Cys Pro Leu Phe
      165             170             175

Ile Ser Glu Val Ser Pro Lys His Leu Arg Gly Thr Leu Val Tyr Cys
      180             185             190

Phe Gln Leu Met Ile Thr Leu Gly Ile Phe Leu Gly Tyr Cys Thr Ser
      195             200             205

Tyr Gly Thr Lys Lys Tyr Ser Asp Ser Arg Gln Trp Arg Ile Pro Leu
      210             215             220

Gly Leu Cys Phe Ala Trp Ala Leu Cys Leu Leu Gly Gly Met Val Arg
      225             230             235             240

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Met Pro Glu Ser Pro Arg Tyr Leu Val Gly Lys Asp Arg Ile Asp Asp
 245 250 255
 Ala Lys Ile Ser Leu Ala Lys Thr Asn Lys Val Ser Pro Glu Asp Pro
 260 265 270
 Ala Leu Tyr Arg Glu Leu Gln Leu Ile Gln Ala Gly Val Glu Arg Glu
 275 280 285
 Arg Leu Ala Gly Lys Ala Ser Trp Gly Ala Leu Ile Thr Gly Lys Pro
 290 295 300
 Arg Ile Leu Glu Arg Val Ile Val Gly Gly Met Leu Gln Ser Leu Gln
 305 310 315 320
 Gln Leu Thr Gly Asp Asn Tyr Phe Phe Tyr Tyr Ser Thr Thr Ile Phe
 325 330 335
 Lys Ser Val Gly Leu Asn Asp Ser Phe Glu Thr Ser Ile Ile Leu Gly
 340 345 350
 Val Ile Asn Phe Ala Ser Thr Phe Val Gly Ile Tyr Ala Ile Glu Arg
 355 360 365
 Leu Gly Arg Arg Leu Cys Leu Leu Thr Gly Ser Val Ala Met Ser Ile
 370 375 380
 Cys Phe Leu Ile Tyr Ser Leu Ile Gly Thr Gln His Leu Tyr Ile Asp
 385 390 395 400
 Gln Pro Gly Gly Pro Thr Arg Lys Pro Asp Gly Asn Ala Met Ile Phe
 405 410 415
 Ile Thr Ala Leu Tyr Val Phe Phe Phe Ala Ser Thr Trp Ala Gly Gly
 420 425 430
 Val Tyr Ser Ile Val Ser Glu Leu Tyr Pro Leu Lys Val Arg Ser Lys
 435 440 445
 Ala Met Gly Phe Ala Asn Ala Cys Asn Trp Leu Trp Gly Phe Leu Ile
 450 455 460
 Ser Phe Phe Thr Ser Phe Ile Thr Asp Ala Ile His Phe Tyr Tyr Gly
 465 470 475 480
 Phe Val Phe Met Gly Cys Leu Val Phe Ser Ile Phe Phe Val Tyr Phe
 485 490 495

Met Ile Tyr Glu Thr Lys Gly Leu Thr Leu Glu Glu Ile Asp Glu Leu
 500 505 510

Tyr Ser Thr Lys Val Val Pro Trp Lys Ser Ala Gly Trp Val Pro Pro
 515 520 525

Ser Asp Glu Glu Met Val Arg Ala Lys Gly Tyr Thr Gly Asp Ile His
 530 535 540

Ala Asp Glu Glu Gln Val
 545 550

<210> 44

<211> 508

<212> DNA

<213> Candida albicans

<400> 44

ttcatgatta tatgatttca tttaatatat tgatttaata tatatatatta attactcata 60
 tagtcgtatt acacctgtag cccaattcat aagggtcatg cggattagtc ttcagcctct 120
 acttcccata atatatctat tatgcatcac taattatagt agggccgacc atagggtcggg 180
 cttacttaaa tagtcgaggg ttgcgttcat tatataacta aataaaaatac cacttgatcat 240
 gaactgacga caacaatgta acgcctgtat atactcgttc aggtaatgag tatatatattca 300
 agaattggta aggtgttagg ggtatcatcc aattaaacag cataatccac tgtacctgta 360
 tataaccgtc taatgtattg catttcatcc gtgaggacgt actagtctgg cgggtgtactt 420
 caagtattaa cgtaccata atgaaagtta taggtttata aaccataac tatcttacat 480
 atacgtagta cacatagttt acggctac 508

<210> 45

<211> 863

<212> DNA

<213> Candida albicans

<400> 45

ctcgtgcata attatcttaa aaccgtagat aagcaaaaat ttatcttatg aaatgttcag 60
 cgataaagaa agaaagaatc aggtaccacg aggagtgttt ttgagaaaaa caactcgtaa 120
 attaataaat ctagtttctc tataacttgaa taatttttga gttttctgga aaagacacct 180
 gttccagttt caaattaaac aagaatgtga aaagaataaa atttgattta ttctagcctg 240
 ttaataatcc aggaaaactc aattttcgta attggcaact tgtccgagtg gtttaaggaga 300
 aagattagaa atcttttggg ctttgccgc gcagggttca gtctgcagt tgtcggtatt 360
 ttttttgggt tactctctat tttaaaattt aaaactaatc aactgaaact ggagtacctg 420
 ccatgatatg agtaataact tttttgatat taaaaatcta tataaaactc cctatttatt 480
 ttttaattta aaccagata ttgtcccaat aatagttttt tgtttgaact tattgctttg 540
 tatgaacctt gttagttaa tctttccaat ttcatactct cttagtgtggc cacatcagt 600
 gtcattgaa taattctgat cttgaagtgt accagatgta ttctgacaaa actgcacacg 660
 gaccagtc atagcattat agatattttg atttaaagt caccgaatat atcgaatatc 720
 tttattggcc atctcatctc atcttcttgc aataaattct taaacgctac tttttctcaa 780

accttattat cccctctagat actctttccaa atcttcaggt tcaaatatca ctttaaccat 840
caatgaacaa ctagggcaaa cag 863

<210> 46

<211> 925

<212> DNA

<213> Candida albicans

<400> 46

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ttgttacgca atgagttacc aattcgggaa gctagtaggg ctaccagagc taggttccag 180
ttaccaattc gggaagctag tagagctacc agagctgggt tccagttacc gatttaggaa 240
gtgtgttgca agcaggggcta ccaaatatgg gtggcaacac atatggtaat aagtgtacc 300
aatgtgggtg caaaaaattt tgccaagtaa tttgtatggc aataacagaa gtgttggcgg 360
attcgaactc aggaatcttt ggtgtgtaaa aaaaaagcaa tagcgactac gctacaagag 420
gcaatcgatt attattataa agtggaagt atatatatgt tgcggggggg gggtaggggc 480
gctgcgcgcc cctgactttg acgggcccga cgcggtttg gggtgtgatg gggcggtaaa 540
taataaggat tctccctccc tttttctct tccccccct cctcctccc ctttccctt 600
ttccccgagt ctacaaatct acaagaggcc cgacggtgga ggcctgaggc cgaaggtcga 660
aggccgacaa agatgggtgg gtgggtggga gggtgtgttc ggggcgtagc cccgagaaaa 720
ttttggaata cagggccagg agggtagggg aaatggggaa aatgggggat ttgggagggga 780
atggggaagg aagaagaaga aaaaagtggg ggaaaggaga agattttttt tgggagaaaa 840
aatttttttt ataccaccga gaagtgtgag aggatacgat ggggtgcgaca gggggtagag 900
ctgttgacaa cgttatatgg gggag 925

<210> 47

<211> 78

<212> PRT

<213> Candida albicans

<400> 47

Met	Gly	Ala	Thr	Cys	Pro	Leu	Arg	Lys	Val	Ala	Thr	His	Arg	Asn	Gly
1				5				10						15	
Leu	Pro	Ile	Trp	Glu	Ala	Ser	Arg	Ala	Thr	Arg	Ala	Thr	Lys	Val	Leu
		20						25						30	
Trp	Glu	Ser	Trp	Val	Gln	Tyr	Thr	Leu	Leu	Arg	Asn	Glu	Leu	Pro	Ile
		35						40						45	
Arg	Glu	Ala	Ser	Arg	Ala	Thr	Arg	Ala	Arg	Phe	Gln	Leu	Pro	Ile	Arg
		50						55						60	
Glu	Ala	Ser	Arg	Ala	Thr	Arg	Ala	Gly	Phe	Gln	Leu	Pro	Ile		
		65						70						75	

<210> 48
 <211> 81
 <212> PRT
 <213> Candida albicans

<400> 48
 Met Gly Tyr Arg Phe Gly Lys Leu Val Gly Leu Pro Glu Leu Pro Lys
 1 5 10 15
 Tyr Cys Gly Arg Val Gly Tyr Ser Thr His Cys Tyr Ala Met Ser Tyr
 20 25 30
 Gln Phe Gly Lys Leu Val Gly Leu Pro Glu Leu Gly Ser Ser Tyr Gln
 35 40 45
 Phe Gly Lys Leu Val Glu Leu Pro Glu Ser Gly Ser Ser Tyr Arg Phe
 50 55 60
 Arg Lys Cys Val Ala Ser Arg Ala Thr Lys Tyr Gly Trp Gln His Ile
 65 70 75 80
 Trp

<210> 49
 <211> 759
 <212> DNA
 <213> Candida albicans

<400> 49
 ctaccaccga aaattccgaa atttcaaaaa ctcaaaatcc ctaaaaacaa actatccaga 60
 gattattgcc atgccctgag gatgagttta gttttttaat ttttgaaaaa tgtccaaaac 120
 tggttgtgct gtataggagg ggtaagaatt tgccattctg cccctttggg tgggtcagtc 180
 aaaaaaagag gtatcactct ggttcaaacg ggaaacaaca gaaaatggga taaaaataat 240
 ctccagacca aacttagtag taacagccat tttagttgta ctggtatacc ctacacaagt 300
 tgtccatttt gtatggggaa ggggaattta gacaaaattt tttttttgaa tttcgctaag 360
 tgtcaagacc cgcaaaagtc accttttttc gttttcaact atggcagagg ctcacctttt 420
 gtctggtgca cagccaaatt gattttgtgg gtgcgactg gaaaaacagt ttgttagtgg 480
 acacgttttt gcagtgtgaa actgcgctcg gaggtactat atgcgaaagc agaaaagaca 540
 attgcaagaa tacagagagt tcttctctgg gctattgcaa tgtgtttaag gccaaagtcga 600
 cgagtgggga gagtctggaa gtgatataca catcacgacc tactttatac gctacgttcg 660
 gcatgggcga gccactgtac ggtggcaagc ctgaacagtc ccacaccaga tatctaacga 720
 ttctgtgtat gggcactgat ggatttagtg gattactag 759

<210> 50
 <211> 902
 <212> DNA

<213> *Candida albicans*

<400> 50

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902

<210> 51

<211> 233

<212> PRT

<213> *Candida albicans*

<400> 51

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Asn His Asn His Val Ala Pro Ile Pro Thr Thr Ala Gly Gln Ser Leu
      20              25              30

Asn Asn Lys Ile Asp Thr Ser Lys Val Thr Ala Leu Asn Met Ala Asn
      35              40              45

Ser Ala Asp Asp Leu Ala Lys Val Phe Lys Asp Ser Thr Lys Lys Tyr
      50              55              60

Gln Ile Lys Pro Ile Ile Lys Ser Asp Ser Asp Glu Gln Met Ile Ile
      65              70              75              80

Asn Ile Pro Phe Leu Asn Gly Ser Val Lys Leu Tyr Ser Ile Ile Leu
      85              90              95

Arg Thr Asn Gly Asp Leu Tyr Cys Pro Lys Thr Ile Lys Leu Phe Lys
      100              105              110

Asn Asp Thr Ser Ile Asp Phe Asp Asn Val Asp Ser Lys Lys Pro Ile

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115 120 125
 Gln Val Leu Thr His Pro Gln Val Gly Val Ala Asn Asn Asp Ser Asp
 130 135 140
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 145 150 155 160
 His Tyr Val Ser Arg His Lys Phe Thr Gly Val Asn Gln Leu Thr Ile
 165 170 175
 Phe Ile Glu Asp Ile Tyr Asp Glu Gly Glu Glu Glu Cys His Leu His
 180 185 190
 Ser Ile Glu Leu Arg Gly Glu Phe Thr Glu Leu Asn Lys Asp Pro Val
 195 200 205
 Ile Thr Leu Tyr Glu Ser Ala Ala Asn Pro Ala Asp His Lys Asn Leu
 210 215 220
 Thr Ile Val Glu Asn Gln Asn Leu Ala
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 <211> 1833
 <212> DNA
 <213> Candida albicans

 <400> 52
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1833

<210> 53

<211> 610

<212> PRT

<213> Candida albicans

<400> 53

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Ile Ser Gly Pro Tyr Gln Glu Glu Asp Thr Pro Ile Lys Arg Leu His
      20              25              30

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```

Ser Ile Pro Ala Ser Thr Ser Glu Asp Glu Asp Glu Leu Asp Pro Glu
      35              40              45

```

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Glu Phe Ile Leu Asn Lys Val Asp Lys Pro Ala Thr Lys Asp Ser His
      50              55              60

```

```

Val Ser Tyr Asn Lys Phe Ser Asp Lys His Ile Ser Asp Glu Gln Leu
      65              70              75              80

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```

Ser His Leu Leu Asp Asn His Lys Pro Asn Leu Val Thr Thr Thr Thr
      85              90              95

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```

Leu Ile Asp Ser Ile Lys Glu Ser Glu Ser Leu Tyr Asn Thr Met Asp
      100              105              110

```

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Ser Leu Met Ile Lys Ser Ile Asn Phe Pro Ala Ala Met Tyr Gln Ser
      115              120              125

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Asn Asp Asn Asn Ser Gln Ser Pro Ile Glu Tyr Leu Ser Asn Arg Val
      130              135              140

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Lys Leu Leu Thr Gln Glu Leu Tyr Glu Asp Ser Val Lys Tyr Gly Lys

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Phe Leu Gln Ser Gly Asn Asn His Ile Tyr Gln Leu Arg Ser Arg Ile	165	170	175
Leu Gln Thr Phe Asp Gln Leu Ser Glu Ser His Tyr Ser Leu Asn Glu	180	185	190
Leu Tyr Asn Lys Asp Met Ser Tyr Ala Glu Thr Leu His Gly Ser Phe	195	200	205
Lys Lys Trp Asp Gln Gln Arg Asn Lys Val Leu Ser Lys Val Lys Ser	210	215	220
Ile Lys Ser Asp Thr Ser Lys His Gly Ala Lys Leu Phe Thr Leu Leu	225	230	235
Asp Glu Val Asn Asp Val Asp Asp Glu Ile Lys Leu Leu Glu Ala Lys	245	250	255
Leu Gln Gln Leu Arg Ser Lys Lys Glu Ile Leu Asn Lys Glu Ile Glu	260	265	270
Asp Thr Ser Ser Val Leu Glu Ser Arg Thr Ala Lys Tyr Val Asp Ile	275	280	285
Phe Lys Asp Leu Glu Asn Lys Gly Arg Ser Ala Ile Thr Asp Phe Leu	290	295	300
Gln Ser Asn Gly Val Pro Glu Lys Glu Ile Asp Thr Ile Val Arg Phe	305	310	315
Ser Pro Val Asp Ile Thr Ile Ser Ser Asn Tyr Ser Ser Lys Lys Glu	325	330	335
Pro Lys Lys Glu Ile His Ile Thr Lys Glu Ser Ile Pro Gln Asn Glu	340	345	350
Ser Ala Ser Lys Pro Ala Asn Thr Pro Ser Ile Gly Met Gln Pro Phe	355	360	365
Ile Ile Pro Glu Ala Glu Ala Asn Thr Lys Thr Pro Asp Leu Gln Ser	370	375	380
Met Asn His Asp His Gly Pro Thr Pro Phe Glu Lys Gly Tyr Ala Met	385	390	395
Gly Thr Gln Asn Ser Thr Ala Leu Lys Asn Lys Met Asn His Ile Met			400

405	410	415
Lys Lys Phe Leu Asp Ser Leu Pro Ile Thr Pro Pro Ser Asn Ile Ser		
420	425	430
Thr Met Pro Ala Thr Ser Arg Ile Lys Val Asp Asp Leu Ser Asn Thr		
435	440	445
Ile Ser Lys Arg Leu Asp Leu Asp Pro Ile Met Val Phe Leu Glu His		
450	455	460
Lys Val Ala Ala Leu His Asp Leu Ala Ile Lys Ser Ser Gln Asn Ala		
465	470	475 480
Ala Leu Phe His Glu Phe Gly Arg Ile Trp Glu Ser Val Thr Lys Leu		
485	490	495
Met Asn Ser Gln Glu Glu Lys Leu Glu Ser Ile Leu Asn Asp Asp Ser		
500	505	510
Asn Ser Lys Leu Val Thr Arg Ile Leu Asn Ser Thr Leu Glu Gln Leu		
515	520	525
Lys Ser Thr Leu Ser Ala Leu Lys Ser Asn Pro Val Thr Ser Gly Ser		
530	535	540
Pro Arg Asp Glu Val Leu Ile Ser Leu Ile Thr Ser Glu Tyr Asn Ala		
545	550	555 560
Ile Glu Gln Ala Val Lys Leu Val Ser Pro Asp Leu Arg Thr Ile Gly		
565	570	575
Glu Leu Asn Ser Ser Gly Gly Leu Pro Pro Ser Ser Ser Lys Pro Thr		
580	585	590
Ser Gln Val Tyr Pro Val Ser Thr Ser Asp Thr Lys Ser Thr Thr Lys		
595	600	605
Met Glu		
610		

<210> 54

<211> 75

<212> PRT

<213> Candida albicans

<400> 54

Met Ser Thr Tyr Phe Ala Val Ser Leu Ser Lys Thr Ser Ser Val Ser
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 Phe Ala Ser Lys Ser Leu Ile Ser Ser Ser Thr Ser Leu Thr Ser Ser
 35 40 45
 Asn Lys Val Asn Asn Leu Ala Pro Cys Leu Leu Val Ser Leu Phe Ile
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 Asp Phe Thr Leu Asp Asn Thr Leu Phe Leu Cys
 65 70 75

<210> 55

<211> 1164

<212> DNA

<213> Candida albicans

<400> 55

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<210> 56

<211> 297

<212> PRT

<213> Candida albicans

<400> 56
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 Lys Arg Tyr Ser Glu Phe Gln Gln Leu Val Ser Asp Leu Ser Arg Asn
 35 40 45
 Leu Gly Ile Asp Ser Arg Asp Phe Pro Tyr Glu Leu Pro Gly Lys Arg
 50 55 60
 Ile Asn Trp Leu Asn Lys Thr Ser Ile Val Glu Glu Arg Lys Val Gly
 65 70 75 80
 Leu Ala Glu Phe Leu Asn Asn Leu Ile Gln Asp Ser Thr Leu Gln Asn
 85 90 95
 Glu Arg Glu Val Leu Ser Phe Leu Gln Leu Pro Ser Asn Phe Arg Phe
 100 105 110
 Thr Lys Asp Met Leu Gln Asn Asn Arg Ala Asp Leu Asp Ser Val Gln
 115 120 125
 Asn Asn Trp Tyr Asp Val Tyr Arg Lys Leu Lys Ser Asp Ile Leu Asn
 130 135 140
 Glu Ser Ser Ser Ser Ile Ser Glu Gln Ile His Ile Arg Asp Arg Ile
 145 150 155 160
 Ser Arg Val Tyr Gln Pro Arg Ile Leu Asp Leu Val Arg Ala Ile Gly
 165 170 175
 Thr Asp Lys Glu Glu Ala Leu Lys Lys Lys Gln Leu Val Ser Gln Leu
 180 185 190
 Gln Glu Ser Ile Asp Asn Leu Leu Val Gln Glu Val Pro Arg Ser Lys
 195 200 205
 Arg Val Leu Gly Gly Ala Val Lys Glu Thr Pro Glu Thr Leu Pro Leu
 210 215 220
 Asn Asn Lys Glu Leu Leu Gln His Gln Val Gln Ile His Gln Asn Gln
 225 230 235 240
 Asp Lys Glu Leu Asp Gln Leu Arg Val Leu Ile Ala Arg Gln Lys Gln
 245 250 255

Ile Gly Glu Leu Ile Asn Ala Glu Val Glu Glu Gln Asn Glu Met Leu
 260 265 270

Asp Arg Phe Asn Glu Glu Val Asp Tyr Thr Ser Ser Lys Ile Lys Gln
 275 280 285

Ala Arg Arg Arg Ala Lys Lys Ile Leu
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<210> 57

<211> 7707

<212> DNA

<213> *Candida albicans*

<400> 57

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<212> PRT

<213> Candida albicans

<400> 58

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Leu Thr Gly Phe His Leu Ser Thr Ile Thr Ile Asn Asn Gly Ile Ser
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Phe Asn Gly Ile Ser Phe His Thr Lys Arg Tyr Leu Ile Ser Val Gly
50 55 60
Ser Leu Arg Phe Arg Leu Trp Gly Asn Ser Lys Met Thr Ile Ile Asp
65 70 75 80
Asp Leu Thr Ile Lys Leu Leu Pro Asn Val Lys Asn Asn Gln Lys Gln
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Asn Thr Gln Glu Lys Arg Asn Asp Tyr Ser Phe Lys Asp Pro Thr Ala
100 105 110
Pro Val Val Asn Ile Phe Pro Gln Asn Arg Ile Gly Lys Tyr Val Val
115 120 125
Ser Arg Leu Ile Arg His Leu Pro Lys Met Asn Leu Glu Leu Arg Gln
130 135 140
Thr Ala Ile Ile Thr Pro Ser Glu Asn Lys Thr Ile Ile Glu Tyr Leu
145 150 155 160
Lys Phe Thr Thr Ser Ser Lys Tyr Ser Lys Arg Ser Asn Glu Lys Ile
165 170 175
Thr Phe Lys Ala Gly Leu Tyr Ile Asn Asn Val Leu His His Leu Lys
180 185 190
Thr Lys Gly Asp Val Ile Lys Pro Phe Gln Ile Gly Gly Ala Ser Phe
195 200 205

Glu Ala Lys Phe Ser Ile Asn Phe Glu Thr Gly Val Leu Asp Asp Leu
 210 215 220
 Lys Thr Arg Val Asn Ile Asn Asp Ser Asp Phe Ser Val Phe Asn Ala
 225 230 235 240
 Ile Lys Tyr Tyr Phe Ile Leu Lys Asp Ser Gln Glu Thr Lys Asn Asn
 245 250 255
 Thr Asn Asn Gln Ser Thr Leu Ser Gln Ala Glu Ile Glu Ala Lys Glu
 260 265 270
 Glu His Lys Leu Gln Arg Leu Glu Asn Thr Phe Lys Ile Ile His Ala
 275 280 285
 Ile Val Ser Glu Ile Asn Leu His Ile Glu Asn Val Lys Ile Ser Glu
 290 295 300
 Ile Pro Phe Val Thr Met Glu Asn Asn Pro Asp Phe Lys Glu Tyr Phe
 305 310 315 320
 Asn Asp Val Arg Pro Ala Thr Cys Leu Glu Met Met Thr Lys Ser Thr
 325 330 335
 Ser Phe Asn Phe Ser Arg Met Tyr Ser Asp Ala Ala Gly Phe Glu Val
 340 345 350
 Leu Phe Asn Ser Lys Arg Asp Arg Pro Tyr His Leu Thr Cys Ser Val
 355 360 365
 Gln Leu Leu Lys Val Phe Phe Ala Ser Arg Val Glu Leu Pro Thr Gly
 370 375 380
 Gln Val Asp Asn Asn Thr Asp Glu Ile Leu Asn Val Pro Asn Phe Ala
 385 390 395 400
 Leu Thr Tyr Lys Thr Asn Ile Leu Asn Gln Val Val Arg Ala Arg Gly
 405 410 415
 Phe Lys Asn Cys Val Val Glu Ile Tyr Phe Ser Ala Ser Thr Pro Ile
 420 425 430
 Leu Asp Leu Asp Thr Arg Gln Leu Ser Ser Leu Leu Tyr Asn Leu Val
 435 440 445
 Leu Leu Lys Lys Trp Lys Thr Ile Lys Lys Leu Glu Lys Leu Leu Glu
 450 455 460

Lys Thr Pro Thr Ser Ser Ser Asp Leu Gln Asp Asp Asp Phe Asp Gly
 465 470 475 480
 Ser Glu Thr Ser Asn Leu Lys Ile His Pro Gly Thr Pro His His Lys
 485 490 495
 Glu Lys Ile Asn Ala Arg Ile Trp Arg Tyr Leu Thr Asp Tyr Tyr Pro
 500 505 510
 His Leu Asp Ile Lys Thr Val Val Glu Gln Pro Arg Leu Val Leu Arg
 515 520 525
 His Cys Glu Pro Lys Lys Asn Thr Gln Ile Leu Thr Phe Ser Tyr Ser
 530 535 540
 Leu Leu Asn Phe Thr Leu Ser Thr Thr Glu Thr Arg Asp Tyr Thr Ser
 545 550 555 560
 Ser Cys Gln Leu Leu Leu Pro Leu Val Thr Tyr Tyr Glu Lys Pro Phe
 565 570 575
 Ser Asp Val Ser Asp Leu His Gly Lys Glu Leu Val Thr Lys Arg Val
 580 585 590
 Ala His Thr Ser Tyr Ile Asp Ile Lys Leu Glu Ile Phe Lys Asn Leu
 595 600 605
 Thr Val Lys Leu Leu Val Asp Val Asp Lys Val Thr Ile Asp Leu Thr
 610 615 620
 Asn Leu Asp Ile Phe Thr Gly Ile His Asn Leu Leu Leu Asp Val Thr
 625 630 635 640
 Gln Ile Ala Glu Thr Asp Leu Glu Leu Gly Val Ile Asn Lys Met Leu
 645 650 655
 Asn Leu Gln Phe Leu Gln Leu Arg His Glu Leu Gln Leu Arg Gln Val
 660 665 670
 Ser Tyr Phe Lys Lys Asn Ile Lys Pro Thr Leu Glu Gln Lys Leu Phe
 675 680 685
 Arg Tyr Leu Pro Lys Trp Leu Thr Arg Ile Asp Leu Lys Val Thr Phe
 690 695 700
 Leu Asn Ile Ser Leu Gly Ser Arg Ser Val Leu Ile Pro Lys Lys Asp
 705 710 715 720

Leu Ser Arg Ala Glu Ser Pro Asp Phe Asp Phe Asp Phe Asp Asp Asp
 725 730 735

His Glu Leu Lys Gln Ile Asp Leu Lys Phe Asp Ser Leu Ser Ile Gly
 740 745 750

Val Ala Lys Asn Ser Lys Thr Ser Gly Glu Ser Thr Pro Ser Thr Val
 755 760 765

Ala Ser Ser Ala Ser Ser Glu Thr Leu Thr Ile Ser Asn His Asp Thr
 770 775 780

Val Tyr Trp Ala Val Asn Ala Thr Leu Glu Lys Leu Lys Leu Ser Ala
 785 790 795 800

Leu Thr Asp Leu Asp Gly Lys Phe Gly Arg Leu Leu Glu Ile Pro Thr
 805 810 815

Ile Lys Thr Asn Val Ser Ala Ile Cys Asp Tyr Tyr Gly Asn Asn Lys
 820 825 830

Leu Ile Thr Asp Val Lys Val Glu Lys Ile Leu Val Asp Tyr Asn Arg
 835 840 845

Tyr Lys Leu Tyr Thr Leu Ile Gly Ser Ile Tyr Leu Ile Arg Glu Phe
 850 855 860

Val Leu Ala Pro Ile Lys Val Ile Lys Ser Lys Val Asn Lys Asp Leu
 865 870 875 880

Thr Lys Phe Asp Ser Asn Leu Ser Pro Asp Pro Asn Ala Ala His Lys
 885 890 895

Thr Thr Ser Ile Leu Asp Phe Leu His Leu Asp Phe Lys Leu Asp Tyr
 900 905 910

Ser Asp Met Ile Leu Cys Leu Ser Lys Asp Phe Lys Val Arg Leu Gln
 915 920 925

Leu Asn Ala Met Gln Ala Ala Tyr Arg Asp Arg Thr Ala Asp Leu Ser
 930 935 940

Ile Thr Phe Leu Arg Gly Leu Ala Glu Ser Pro Leu Val Ala Asn Lys
 945 950 955 960

Trp Cys Arg Leu Leu Cys Leu Asp Thr Leu Lys Phe Lys Ser Glu Ile
 965 970 975

Thr Ser Ser Ile Lys Asp Leu Ser Ile Glu Leu Asp Ser Asp Ala Val
 980 985 990

Arg Phe Ile Gln Pro His Gln Phe Val Val Tyr Lys Phe Phe Asp Asn
 995 1000 1005

Ile Ser Ile Thr Val Lys Leu Val Lys His Leu Val Lys Leu Leu Lys
 1010 1015 1020

Asp Glu Ser Thr Lys Glu Asp Leu Asn Ile Val His Pro Asn Leu Gln
 1025 1030 1035 1040

Lys Ala Lys Leu Leu Pro Phe Ile Arg Phe Lys Ser Lys Ser Leu Lys
 1045 1050 1055

Phe Cys Val Glu Asp Asp Pro Phe Glu Thr Glu Leu Gly Met Ile Tyr
 1060 1065 1070

Gln Leu Gly Lys Val Glu Gln Arg Lys Arg Leu Glu Leu Tyr Asn Leu
 1075 1080 1085

Phe Glu Thr Lys Ala Ser Thr Ser His Ile Asp Thr Glu Glu Tyr Phe
 1090 1095 1100

Asp Asn Leu Ser Arg Leu Asn Arg Thr Ile Ser Gln Ser Trp Ile Arg
 1105 1110 1115 1120

Lys Val Asn Val Tyr Lys Ser Lys Leu Arg Ser Glu Ile Ile Ala Asn
 1125 1130 1135

Lys Asp Tyr Leu Leu Gly Asn Glu Val Lys Leu Asp Glu Ser Leu Asn
 1140 1145 1150

Asp Asp Val Val Thr Tyr Ala Tyr Ala Ser Pro Leu Phe Ser Val Tyr
 1155 1160 1165

Met Asp Lys Phe Gln Ile Asp Ile Ser Lys Pro Lys Phe Asn Ile Asp
 1170 1175 1180

Glu Val Ala Asn Phe Ile Tyr Asp Phe Gly Gln Gly Val Pro Lys Thr
 1185 1190 1195 1200

Thr Glu Tyr Thr Leu Leu Ile Pro Ile Tyr Met Ala Leu Gln Leu Gly
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Glu Leu Arg Met His Leu Arg Asp Tyr Pro Leu Pro Leu Leu His Ser
 1220 1225 1230

Pro Arg Asn Lys Asp Met Asp Glu Thr Ser Phe Lys Leu Asn Gly His
 1235 1240 1245
 Leu Val Ile Ser Glu Ala Phe Ala Lys Ala Ile Glu His Met Arg Gln
 1250 1255 1260
 Ile Asp Val Pro Leu Val Pro Glu His Lys His Lys His Lys Gln Leu
 1265 1270 1275 1280
 Asn Lys Phe Glu Phe Leu Val Met Glu Lys Thr Leu Ala Ser Val Lys
 1285 1290 1295
 Leu Cys Thr Asp Leu Glu Cys Val Phe Asn Ser Asn Tyr Pro Thr Arg
 1300 1305 1310
 Ile Val Trp Gly Ala Ser Tyr Asn Phe Gly Ile Gln Gln Met Met Ala
 1315 1320 1325
 Asn Phe Asp Arg Phe Ser Lys Pro Pro Val Asp Pro Ser Thr Lys Leu
 1330 1335 1340
 Gly Phe Trp Asp Lys Leu Lys Tyr Ile Leu His Gly Lys Cys Gln Ile
 1345 1350 1355 1360
 Arg Thr Arg Lys Ser Leu Glu Val Ala Phe Lys Gly Ser Arg Asp Pro
 1365 1370 1375
 Tyr Asp Leu Phe Thr Thr Ala Gly Gly Phe Val Leu Ser Phe Arg Lys
 1380 1385 1390
 Asn Val Val Trp Asp Ile Asn Lys Asp Asp Asn Ser Lys Asn Tyr Phe
 1395 1400 1405
 Asp Ile Thr Ala Asp Lys Val Ser Trp Tyr Ile Pro Asn Tyr Leu Ala
 1410 1415 1420
 Gly Pro Leu Leu Ala Trp Thr Arg Ser Ser Lys Asn Ser Ile Tyr Leu
 1425 1430 1435 1440
 Pro Asn Ser Pro Asn Val Val Asn Ser Cys Phe Ala Tyr Tyr Leu Gln
 1445 1450 1455
 Asp Phe Thr Gly Gln Ala Asp Phe Asp His Ala Ala Arg Val Phe Glu
 1460 1465 1470
 Arg Asn Val Val Asn Leu Ser Gly Gly Ile His Phe Gln Val Gly Phe
 1475 1480 1485

Leu Leu Glu Arg Lys Asp Thr Asn Gly Lys Arg Thr Asp Glu Phe Lys
 1490 1495 1500

Pro His Tyr Glu Val Gln Leu Phe Asp Pro Lys Tyr Cys Glu Lys Gly
 1505 1510 1515 1520

His Asp Ser Tyr Ala Gly Phe Arg Ser Gln Phe Ile His Met Ala Ile
 1525 1530 1535

Ser Leu Glu Ser Thr Asn Ser Ser Ser Tyr Asn Thr Ile His Leu Ser
 1540 1545 1550

Pro Gly Thr Phe Gln Gln Phe Phe Asp Trp Trp Lys Leu Phe Ala Ser
 1555 1560 1565

Asn Met Gln Leu Pro Ile Arg Arg Gly Lys Met Phe Gly Glu Ala Lys
 1570 1575 1580

Glu Ser Val Lys Phe Ser Gln His Leu Phe Thr Asn Lys Phe Ser Phe
 1585 1590 1595 1600

Met Leu Lys Ser Leu Phe Ile Ala His Val Tyr Arg Asp Glu Ile Val
 1605 1610 1615

Asp Ile Asn Asn Asp Arg Ile Glu Ser Ile Gly Leu Arg Ala Lys Val
 1620 1625 1630

Asp Asp Phe Met Val Asp Leu His Gln Arg Lys Glu Pro Ala Thr Leu
 1635 1640 1645

Tyr His Glu Glu Leu Ser Lys Asn Glu Lys Val Met Lys Met Asn Phe
 1650 1655 1660

Asp Leu Gly Glu Val Val Leu Ser Gly Ile Asp Leu Arg Val Met His
 1665 1670 1675 1680

Val Ser Phe Leu Gln Asn Leu Tyr Thr Gln Ser His Ser Asn Ser Gly
 1685 1690 1695

Asp Ala Lys Ser Thr Tyr Asn Ile Tyr Asp Asn Asp His Arg Trp Phe
 1700 1705 1710

Asp Ile Met Asp Phe Gln Glu Ala Phe Leu Thr Ser Ile Lys Asp Cys
 1715 1720 1725

Val Arg Thr Val Asp Ile Tyr Pro Leu Met Tyr Leu Gln Arg Phe Phe
 1730 1735 1740

Tyr Glu Arg Asp Thr His Gly Gly Lys Ser Glu Asp Glu Thr Ala Phe
 1745 1750 1755 1760
 Gly Lys Glu Val Ile His Lys Cys Asn Leu Gly Ala Met Asn Pro Leu
 1765 1770 1775
 Glu Thr Arg Leu Asn Val Leu Val Gln Arg Leu Asn Ala Leu Gln Glu
 1780 1785 1790
 Gln Val Lys Lys Leu Ser Lys Thr Ser Ala Pro Glu Pro Val Ala Asp
 1795 1800 1805
 Leu Lys Lys Arg Ile Ser Phe Leu Gln Lys Glu Ile Ser Thr Thr Lys
 1810 1815 1820
 Ala Ser Val Lys Ser Lys Met Arg Arg Thr Ser Thr Ile Asn Gly Met
 1825 1830 1835 1840
 Asn Asn Ser Glu Asn Tyr His Asn Lys Phe Thr Phe Tyr Asn Met Leu
 1845 1850 1855
 Leu Lys Trp Asn Phe Asn Cys Arg Asn Leu Thr Leu Lys Tyr Ile His
 1860 1865 1870
 Phe Val Lys Leu Lys Ser Gln Leu Arg Asn Tyr Leu Ser His Lys Ser
 1875 1880 1885
 Ile Glu Thr Leu Glu Lys Met Met Asp Ser Val Asn Ala Tyr Asn Asp
 1890 1895 1900
 Lys Asp Asp Leu Ser Ser Thr Ser Glu Ile Ile Arg Arg Phe Thr Ser
 1905 1910 1915 1920
 Glu Gly Val Lys Ser Gln Thr Ser Thr Ser Lys Asp Ile Thr Ser Gln
 1925 1930 1935
 Gln Lys Leu Asp Asn Phe Asn Thr Ile Leu Arg Glu Thr Arg Pro Asp
 1940 1945 1950
 Glu Lys Val Val Glu Asp Tyr Leu Ile Asp Val Ile Ala Pro Gln Ile
 1955 1960 1965
 Gln Leu Gln Ser Glu Asp Tyr Pro Asp Ser Val Val Leu Ile Ser Thr
 1970 1975 1980
 Pro Ser Ile Lys Gly Lys Ile Leu Ser Ile Met Asp Ser Arg Asn Asn
 1985 1990 1995 2000

Ala Asn Gln Ile Leu Leu Glu Thr Arg Tyr Gly Ile Leu Leu Lys Asp
 2005 2010 2015

Ala Asn Val Phe Val Leu Asn Lys Glu Asp Ile Val Gly Cys Pro Asp
 2020 2025 2030

Met Leu Ser Ile Ser Asn Pro Tyr Gly Ala Lys Ser Asn Trp Pro Pro
 2035 2040 2045

Trp Leu Gly Thr Glu Ile Thr Gln Asn Gly Lys Trp Ala Gly Ala Asn
 2050 2055 2060

Asn Leu Leu Ile Glu Lys Leu Ser Val Met Thr Met Cys Tyr Glu Ser
 2065 2070 2075 2080

Glu Ile Leu Ser Ser Lys Leu Ser Pro Asn Ala Gln Asp Ser Asp Gln
 2085 2090 2095

Glu Glu Gln Glu Asn Tyr Asn Asp Asp Asn Ser Lys Gln Ala Pro Leu
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Arg Leu Gly Ile Asp Met Pro Ser Val Val Ile Thr Ser Thr Ser Ser
 2115 2120 2125

Gln Tyr Phe Thr Leu Tyr Val Ile Ile Val Ser Leu Leu Phe Tyr Ser
 2130 2135 2140

Glu Pro Met Ser Lys Val Ile His Lys Lys Ile Glu Lys Met Lys Phe
 2145 2150 2155 2160

Ser Ile Asp Phe Glu Asp Leu Gly Ala Leu Thr Ser Arg Leu Thr Lys
 2165 2170 2175

Met Gln Gln His His Lys Leu Leu Lys Val Leu Ser Asn Asn Tyr Ser
 2180 2185 2190

Phe Arg Gln Gly Lys Leu Asn Asn Glu Asp Leu Asn Asn Tyr Leu Gln
 2195 2200 2205

Val Asn Leu Glu Arg Gly Glu Ile Ala Ser Asp Ile Tyr Leu Leu Leu
 2210 2215 2220

Arg Thr Leu Leu Thr Gly Asp Phe Ala Ser Asp Thr Ser Asn Asn Leu
 2225 2230 2235 2240

Ser Met Xaa Trp Leu Ile Arg Ala Asp Glu Ile Ile Leu Gln Ile Leu
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Glu Asp Asp Arg Thr Pro Ile Met Asp Leu Ala Leu Ala Gln Gly Met
 2260 2265 2270

Tyr Thr Arg Lys Glu Leu Glu Ser Gly Ser Asn Ile Asn Lys Leu His
 2275 2280 2285

Ile Gly Thr Met Arg Gly Phe Asn Leu Ile Glu Ser Ala Arg Tyr Pro
 2290 2295 2300

Asp Phe Ile Lys Pro Ile Thr Glu Ser Ser Ser Gln Asn Leu Ile Glu
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Leu Ala Trp Thr Met Asn Lys Ser Val Gly Gly Ile Lys Ile Ile Glu
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Asn Val Phe Val Asn Ala Ala Pro Leu Asn Ile Lys Leu Asp Glu Ile
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Thr Gly Asp Lys Leu Met Lys Phe Ile Thr Tyr Ser Asn Ser Gly Asn
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Leu Glu Asp Ser Lys Ile Ile Ala Val Ser Asn Glu Lys Asn Lys Asp
 2370 2375 2380

Asn Ile Lys Asp Asn Ser Glu Asp Glu Asp Tyr Gly Leu Ile Thr Glu
 2385 2390 2395 2400

Asn Glu Gly Ile Asn Lys Gly Pro Lys Phe Glu Glu Met Ser Gln Ser
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Ser Asn Met Lys Arg Ser Leu Thr Met Leu Ser Ser Lys Lys Ser Ser
 2420 2425 2430

Ser Ser Ala Ser Ser Asn Asp Glu Ile Glu Asp Asn Glu Asp Val Glu
 2435 2440 2445

Lys Met Ile Glu Arg Ser Lys Lys Tyr Phe Ser Val Val Ser Leu Asn
 2450 2455 2460

Val Asn Ala Ile Thr Leu Glu Val Thr Leu Lys Leu Asn Lys Gly Phe
 2465 2470 2475 2480

Lys Arg Ile Leu Asn Val Asn Asp Phe Arg Ile Asp Leu Pro Glu Phe
 2485 2490 2495

Asn Ile Thr Asn Glu Ile Val Ser Tyr Met Asp Ile Ser Lys Met Leu
 2500 2505 2510

Gln Ser Met Ile Thr Lys Met Ile Leu Gly His Val Gly Arg Leu Leu
 2515 2520 2525

Gly Asn Lys Met Lys Ala Thr Lys Gly Lys Ser Lys Lys Ile Met Lys
 2530 2535 2540

Lys Arg Lys Arg Ile Arg Ser Ile Ser Asp Val Arg Lys Glu Ile His
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Val Ser Thr Glu Arg Gly Ala Asp
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<211> 2196

<212> DNA

<213> Candida albicans

<400> 59

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 agatcaagtc ttccaataga tgaaacgtct cattcaagaa gactttcttt tgaagctcaa 660
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 aatgatcaac atgatgatcg tccaaacttt aaaaatttgg atcaattagt tcagaaaaga 1740

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 agatcaaaac caactccgt tgaaccaat gagtaa 2196

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<211> 731

<212> PRT

<213> Candida albicans

<400> 60

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Asp Gly Phe Asn Gln His His Leu Gly Asp Pro Val Ile Ser Gly Pro
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Pro Tyr Ile Ile Lys Leu Leu Asn Leu Pro Val Thr Ala Asn Asp Ser
 35 40 45

Phe Val Gln Asp Leu Phe Gln Ser Arg Phe Thr Pro Tyr Val Lys Phe
 50 55 60

Lys Ile Val Thr Asp Pro Ala Ser Asn Ile Leu Glu Thr His Val Ile
 65 70 75 80

Arg Gln Val Ala Phe Val Glu Leu Glu Ser Ala Ser Asp Met Ser Lys
 85 90 95

Ala Leu Lys Trp His Asp Leu Tyr Tyr Lys Thr Asn Arg Arg Val Thr
 100 105 110

Val Glu Val Ala Asp Phe Asn Asp Phe Gln Asn Cys Ile Lys Phe Asn
 115 120 125

Gln Glu His Glu Arg Glu Ile Met Gln Ile Gln Gln Glu Phe Ile Ala
 130 135 140

Gln Lys Gln Gln Gln Arg Gln Pro Arg His Met Ala Leu Leu Asp Glu
 145 150 155 160

Phe Glu Arg Asn Gln Arg Gly Pro Gly Ser Pro Leu His Gln Asn His
 165 170 175

Asp His His Asn Pro His Pro Gln Gln Gln Gln His His His Phe Asn
 180 185 190
 Pro Asn Leu Asn Arg Pro Ser Gly Arg Ser Ser Leu Pro Ile Asp Glu
 195 200 205
 Thr Ser His Ser Arg Arg Leu Ser Phe Glu Ala Gln Leu His Pro His
 210 215 220
 Gln Gln Thr His Gly Gln Arg Ile Arg Gln Pro Ser Phe Asp Asn Ala
 225 230 235 240
 Phe Pro Asp Thr Pro His Pro Pro Phe Gly Gly Gly Gly Gly Met Arg
 245 250 255
 Gln Gln Ile His Pro Thr Asn Gln Pro Ala Val Pro Ser Ser Ala Pro
 260 265 270
 Ala Ser Lys Pro Phe Val Thr Pro Ile Ser Ser Ala Ser Thr Ser Ser
 275 280 285
 Arg Pro Ile Ser Asn Pro Phe Gly Ala Ala Lys Pro Val Asp Thr Leu
 290 295 300
 Ser Lys Gln Gln Glu Ile Glu Lys Lys Leu Ile Asn Leu Asn Lys Thr
 305 310 315 320
 Thr Val Gln Thr Leu Gly Asp Val Glu Thr Pro Glu Glu Val Gln Ala
 325 330 335
 Thr Ile Lys Lys Phe His Glu Asn Gly Ser Pro Lys Leu Arg Arg Ala
 340 345 350
 Ser Val Gly Thr Pro Arg Arg Leu Ser Ser Glu Lys Arg Pro Ser Val
 355 360 365
 Ser Ile Leu Arg Arg Asp Leu Pro Glu Arg Gln Gln Pro Pro Pro Pro
 370 375 380
 Pro Gln Gln Gln Gln Gln Gln Gln Pro Pro Gln Gln Gln Asp Gln Asn
 385 390 395 400
 Thr Lys Gln Thr Ala Leu His Gln Pro Asp Gln Leu Gln Asn His Ser
 405 410 415
 Ser Asn Ile Ser Ser Thr Gln Pro Ser Gly Glu Ser Pro Leu Ala Glu
 420 425 430

Thr Gln Ser Leu Ser Thr Asn Pro Tyr Thr Ser Asn Gly Thr Gly Lys
 435 440 445
 Ser Leu Ala Gln Leu Leu Ser Glu Gln Ser Asp Ile Met Ser Ala Pro
 450 455 460
 Pro Ile Thr Gly Lys Lys Thr Pro Arg Ser Asn Ser Asn Thr Lys Lys
 465 470 475 480
 Pro Val Val Ala Ala Lys Pro Val Ile Leu Lys Lys Lys Thr Pro Thr
 485 490 495
 Ser Pro Pro Val Gln Arg Ile Asp Leu Thr Ile Lys Glu Ser Glu Tyr
 500 505 510
 Leu Lys Lys Gln Asp Glu Thr Asp Asp Leu Ile Asp Ala Asn Val Glu
 515 520 525
 Thr Lys Leu Glu Lys Leu Asp Leu Asn Ser Glu Thr Leu Ser Glu Asn
 530 535 540
 Gly Thr Lys Glu Ser Thr Lys Thr Arg Ile Asp Asn Pro Lys Arg Glu
 545 550 555 560
 Asn Asp Gln His Asp Asp Arg Pro Asn Phe Lys Asn Leu Asp Gln Leu
 565 570 575
 Val Gln Lys Arg Asn Asp Ser Arg Ala Ser Ser Ser Ser Ser Asn Ser
 580 585 590
 Arg Arg Phe Glu Phe Ile Arg Gly Leu Lys Glu Glu Asn Glu Arg Val
 595 600 605
 Pro Ser Pro Ser Ser Ser Ser Ser Ser Ser Ser Ala Thr Lys Thr Ser
 610 615 620
 Gln Asn Asn Phe Glu Lys Ser Ser Glu Ser Ala Ile Ser Arg Thr Asp
 625 630 635 640
 Asp Gln Gln Asp Leu Ser Ser Thr Asn Thr Gly Ser Glu Gly Arg Met
 645 650 655
 Trp Glu Arg Gly Arg Gly Arg Gly Arg Gly Phe Ser Phe Arg Ser
 660 665 670
 Arg Gly Gly Phe Arg Gly Arg Gly Ala Gly Phe Arg Gly Ser Gly Arg
 675 680 685

Gly Gly Pro Arg Arg Arg Gly Gly Asn Gly Ala Ser Gly Ala Gly Gly
 690 695 700

Thr Ala Ser Gly Ser Thr Gly Ser Ala Asn Tyr Asn Leu His Tyr Val
 705 710 715 720

Arg Ser Lys Pro Thr Pro Val Glu Thr Asn Glu
 725 730

<210> 61

<211> 1483

<212> DNA

<213> Candida albicans

<400> 61

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ctcactcaaa gagttcaaac catgggatag cagtgttttg tatgagacgt tactacgatc 180
agtattaact actttgatcg aacttttggg catagacaat ccaccagtt atctacacct 240
caccaccaac aatgatagta taggtgattt gaaaataaaa tactatggaa atgcattaag 300
caagtcaatc aacggtcata gcatgttgca atatcttgaa tcaaagcatg tatcgatatt 360
acaggccgtg gttgagatta ttaatacgcg atcatataga atcaaagagt cttattctgc 420
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atctaactca gaggattata tattgcagtg cttgatgtac gagaccaat tttaccaagg 540
aattgttgat aatgttttaa ctgccgatga caccgaaaaa ttggctagtt ttttggggac 600
acgactatct gaagaagatt cgatgttttag ctatagggat atagattatc cactagagtt 660
aaacattaat aatgaatctc ttgaaaagat atataaaatt ttcttaggag tcattggcac 720
caaaagattc gatatcaagg aggttgcgtc tgctgttggt ggtgtgtata aacgacacca 780
gagaatagat cattttgaaa agttggattc agatgagatt ttgggaaagt ttttcagaaa 840
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<210> 62

<211> 468

<212> PRT

<213> Candida albicans

<400> 62

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 1 5 10 15
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 20 25 30
 Leu Arg Ser Val Leu Thr Thr Leu Ile Glu Leu Leu Gly Ile Asp Asn
 35 40 45
 Pro Pro Ser Tyr Leu His Leu Thr Thr Asn Asn Asp Ser Ile Gly Asp
 50 55 60
 Leu Lys Ile Lys Tyr Tyr Gly Asn Ala Leu Ser Lys Ser Ile Asn Gly
 65 70 75 80
 His Ser Met Leu Gln Tyr Leu Glu Ser Lys His Val Ser Ile Leu Gln
 85 90 95
 Ala Val Val Glu Ile Ile Asn Thr Arg Ser Tyr Arg Ile Lys Glu Ser
 100 105 110
 Tyr Ser Ala Val Phe Lys Asp Val Ser His Leu Phe Glu Lys Leu Leu
 115 120 125
 Lys Glu Arg Tyr Glu Ala Glu Ser Asn Leu Glu Asp Tyr Ile Leu Gln
 130 135 140
 Cys Leu Met Tyr Glu Thr Gln Phe Tyr Gln Gly Ile Val Asp Asn Val
 145 150 155 160
 Leu Thr Ala Asp Asp Thr Glu Lys Leu Ala Ser Phe Leu Gly Thr Arg
 165 170 175
 Leu Ser Glu Glu Asp Ser Met Phe Ser Tyr Arg Asp Ile Asp Tyr Pro
 180 185 190
 Leu Glu Leu Asn Ile Asn Asn Glu Ser Leu Glu Lys Ile Tyr Lys Ile
 195 200 205
 Phe Leu Gly Val Ile Gly Thr Lys Arg Phe Asp Ile Lys Glu Val Ala
 210 215 220
 Ser Ala Val Val Gly Val Tyr Lys Arg His Gln Arg Ile Asp His Phe
 225 230 235 240
 Glu Lys Leu Asp Ser Asp Glu Ile Leu Gly Lys Phe Phe Arg Asn Ile
 245 250 255

Leu Pro Gln Ser Phe Gln Ser Val Thr Asn Lys Val Phe Arg Glu Phe
 260 265 270
 His Lys Glu Val Asp Asp Pro Pro Ser Asp Val Leu Asp Gln Leu Asp
 275 280 285
 Asn Ile Val Asp Asp Phe Ile Ala Val Gly Ile Glu Gly Val Asp Leu
 290 295 300
 Gly Phe Pro Ala Leu Phe Arg His Tyr Ile Lys Phe Met Asn Glu Ile
 305 310 315 320
 Phe Pro Thr Val Val Glu Asp Ala Asp Arg Asp Phe Val Ala Arg Ile
 325 330 335
 Asn Ser Leu Ile Ala Gln Val Leu Glu Phe Lys Asp Asp Glu Lys Ser
 340 345 350
 Cys Asp Ile Asn Gln Val Val Ser Glu Phe Val Ser Leu Gln Ser Leu
 355 360 365
 Leu Leu Lys Asn Asn Tyr Leu Ser Pro Ser Thr Leu Leu Met Arg Ala
 370 375 380
 Ser Thr His Asp Tyr Tyr Lys Asn Leu Gln Ile Val Lys Ile Thr Phe
 385 390 395 400
 Asp Gly Trp Asn Glu Asn Ser Lys Arg Ile Leu Lys Leu Glu Asn Ser
 405 410 415
 Gly Phe Leu Gln Ser Lys Thr Leu Pro Lys Tyr Leu Lys Leu Trp Tyr
 420 425 430
 Ser Lys Ser Met Lys Leu Asn Glu Leu Cys Asn Arg Val Asp Glu Phe
 435 440 445
 Tyr Asn Gly Glu Leu Cys Arg Lys Val Trp His Cys Trp Arg Ala Gln
 450 455 460
 Gln Arg Cys Leu
 465

<210> 63

<211> 715

<212> DNA

<213> Candida albicans

<400> 63

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 atatattggt tttcatcaca acagttcata tcgccataga ccatttttaa tcttaagggt 180
 gataccagtt aattgttgat ttctctgtta tagaccctgt ctaaactctgt ctattttctgg 240
 tatcgaatca aaatgtcgct cataatgtgc atgtcgcaaa gatgtcgtaa agttttgatt 300
 tcatactcat cttaaatttt ttttagtgat tggcattttg ttctttcaca tagtttttat 360
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 atttaaatca aaaaagaaat ttatagatcg tcgagaagcc aagtctcaag atataaaacg 480
 tgcattaacc catagggcta gattaagaaa gaactatttc aaactattag aaaaagaagg 540
 gttacaagag gagaggaagc ctgaagatga gaacgatata agaccaacca agaagaaggg 600
 aataaatttt gaagaacgtg cagccattgt gaaacaacgt aaagaggaaa aacgtaaatt 660
 caaactagca agtgtagaag caaaattgga aaagattgaa tctaattcga aagaa 715

<210> 64

<211> 106

<212> PRT

<213> Candida albicans

<400> 64

Met His Pro Asn Asn Lys Asn Ser Phe Lys Ser Lys Lys Lys Phe Ile
 1 5 10 15
 Asp Arg Arg Glu Ala Lys Ser Gln Asp Ile Lys Arg Ala Leu Thr His
 20 25 30
 Arg Ala Arg Leu Arg Lys Asn Tyr Phe Lys Leu Leu Glu Lys Glu Gly
 35 40 45
 Leu Gln Glu Glu Arg Lys Pro Glu Asp Glu Asn Asp Ile Arg Pro Thr
 50 55 60
 Lys Lys Lys Gly Ile Asn Phe Glu Glu Arg Ala Ala Ile Val Lys Gln
 65 70 75 80
 Arg Lys Glu Glu Lys Arg Lys Phe Lys Leu Ala Ser Val Gln Ala Lys
 85 90 95
 Leu Glu Lys Ile Glu Ser Asn Ser Lys Glu
 100 105

<210> 65

<211> 147

<212> DNA

<213> Candida albicans

<400> 65

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 accaatggaa tcatttccca acgtatg 147

<210> 66

<211> 49

<212> PRT

<213> Candida albicans

<400> 66

Met Lys Ile Ser Pro Glu Thr Val Asn Lys Leu Gln Ser Asp Ala Ser
 1 5 10 15

Cys Ile Arg Asn Ile Cys Ile Leu Ala His Val Asp His Gly Lys Thr
 20 25 30

Ser Leu Ser Asp Ser Leu Leu Ala Thr Asn Gly Ile Ile Ser Gln Arg
 35 40 45

Met

<210> 67

<211> 3393

<212> DNA

<213> Candida albicans

<400> 67

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 ttcacacctg aaaagaataa tgtaatatat gcctcggcaa tagatggatg ggcattttca 480
 gtcaatacat ttgccaaaat atacctgaaa aaattagggt tctctcaaca agcattgtca 540
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 gtttgggctg tttatgaaaa ctgtgttatt gaaagaaatc aagacaagtt ggaaaaaatc 720
 attgagaaat taggggccaa aatcaccctt cgtgatttgc gatccaaaga ttacaagaac 780
 ttgctaaact tgattatgtc tcagtggatt cctttgagtc atgccatatt ggggtcagtg 840
 attgaatact tgccaagccc cattgttgct cagcgtgaaa gaatagacaa gattttggat 900
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3393

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<210> 68

<211> 497

<212> PRT

<213> *Candida albicans*

<400> 68

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1

5

10

15

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 Val Ser Thr Ser Ser Arg Leu Cys Asp Gly Ala Val Val Leu Val Asp
 35 40 45
 Val Val Glu Gly Val Cys Ser Gln Thr Val Asn Val Leu Arg Gln Cys
 50 55 60
 Trp Ile Asp Lys Leu Lys Pro Leu Leu Val Ile Asn Lys Ile Asp Arg
 65 70 75 80
 Leu Ile Thr Glu Trp Lys Leu Ser Pro Leu Glu Ala Tyr Gln His Ile
 85 90 95
 Ser Arg Ile Ile Glu Gln Val Asn Ser Val Ile Gly Ser Phe Phe Ala
 100 105 110
 Gly Asp Arg Leu Glu Asp Asp Leu Asn Trp Arg Glu Ala Gly Ser Val
 115 120 125
 Gly Glu Phe Ile Glu Lys Ser Asp Glu Asp Leu Tyr Phe Thr Pro Glu
 130 135 140
 Lys Asn Asn Val Ile Phe Ala Ser Ala Ile Asp Gly Trp Ala Phe Ser
 145 150 155 160
 Val Asn Thr Phe Ala Lys Ile Tyr Ser Lys Lys Leu Gly Phe Ser Gln
 165 170 175
 Gln Ala Leu Ser Lys Thr Leu Trp Gly Asp Phe Tyr Leu Asp Met Lys
 180 185 190
 Asn Lys Lys Ile Ile Pro Gly Lys Lys Leu Lys Asn Asn Ser Asn Ser
 195 200 205
 Leu Lys Pro Leu Phe Val Ser Leu Ile Leu Asp Gln Val Trp Ala Val
 210 215 220
 Tyr Glu Asn Cys Val Ile Glu Arg Asn Gln Asp Lys Leu Glu Lys Ile
 225 230 235 240
 Ile Glu Lys Leu Gly Ala Lys Ile Thr Pro Arg Asp Leu Arg Ser Lys
 245 250 255
 Asp Tyr Lys Asn Leu Leu Asn Leu Ile Met Ser Gln Trp Ile Pro Leu
 260 265 270

Ser His Ala Ile Leu Gly Ser Val Ile Glu Tyr Leu Pro Ser Pro Ile
 275 280 285
 Val Ala Gln Arg Glu Arg Ile Asp Lys Ile Leu Asp Glu Thr Ile Tyr
 290 295 300
 Ser Ala Val Asp Ser Glu Ser Asp Lys Ser Lys Leu Val Asp Pro Ser
 305 310 315 320
 Phe Val Lys Ala Met Gln Glu Cys Asp Ser Ser His Pro Glu Thr His
 325 330 335
 Thr Ile Ala Tyr Val Ser Lys Leu Leu Ser Ile Pro Asn Glu Asp Leu
 340 345 350
 Pro Lys Ala Ser Asn Ala Ala Thr Gly Gly Leu Thr Ala Asp Glu Ile
 355 360 365
 Gln Glu Arg Gly Arg Ile Ala Arg Glu Leu Ala Lys Lys Ala Ser Glu
 370 375 380
 Ala Ala Ala Leu Ala Gln Glu Gly Ser Lys Asn Glu Asp Glu Phe Ala
 385 390 395 400
 Ile Lys Pro Lys Lys Asp Pro Phe Glu Trp Glu Phe Glu Glu Asp Asp
 405 410 415
 Phe Glu Asn Glu Glu Asp Glu Ser Asp Ala Asn Ala Val Glu Glu Ser
 420 425 430
 Thr Glu Thr Ile Val Gly Phe Thr Arg Ile Tyr Ser Gly Ser Leu Ser
 435 440 445
 Arg Gly Gln Lys Leu Thr Val Ile Gly Pro Lys Tyr Asp Pro Ser Leu
 450 455 460
 Pro Arg Asp His Gln Thr Asn Phe Glu Gln Ile Thr Asn Glu Val Glu
 465 470 475 480
 Ile Lys Asp Leu Phe Leu Ile Met Gly Arg Glu Leu Val Arg Met Glu
 485 490 495
 Lys

<210> 69

<211> 467

<212> PRT

<213> Candida albicans

<400> 69

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 20 25 30
 Asn Leu Ala Ser Thr Ser Thr Leu Ile His Asn Lys Pro Ile Met Lys
 35 40 45
 Ile Ala Val Glu Pro Thr Asn Pro Ile Lys Leu Ala Lys Leu Glu Arg
 50 55 60
 Gly Leu Asp Leu Leu Ala Lys Ala Asp Pro Val Leu Glu Trp Tyr Val
 65 70 75 80
 Asp Asp Glu Ser Gly Glu Leu Ile Val Cys Val Ala Gly Glu Leu His
 85 90 95
 Leu Glu Arg Cys Leu Lys Asp Leu Glu Glu Arg Phe Ala Lys Gly Cys
 100 105 110
 Glu Val Thr Val Lys Glu Pro Val Ile Pro Phe Arg Glu Gly Leu Ala
 115 120 125
 Asp Asp Lys Ile Ser Thr Asn Thr Asn Asn Asn Asn Asp Asp Asn Glu
 130 135 140
 Asp His Glu Leu Asp Glu Asn Glu Asp Glu Leu Ala Asp Leu Glu Phe
 145 150 155 160
 Asp Ile Ser Pro Leu Pro Leu Glu Val Thr Gln Phe Leu Ile Glu Asn
 165 170 175
 Glu Thr Ile Ile Ala Glu Ile Val Asn Asn Lys Gln Asp Thr His Glu
 180 185 190
 Ile Arg Asn Asp Phe Ile Glu Lys Phe Ala Thr Ile Ile Asp Asn Ser
 195 200 205
 Asn Leu Ala Thr Gln Phe Pro Asp Thr Lys Ser Phe Ile Asn Asn Ile
 210 215 220
 Ile Cys Phe Gly Pro Lys Arg Val Gly Pro Asn Ile Phe Ile Glu Asp
 225 230 235 240

Tyr Gly Leu Asn Lys Phe Arg His Leu Leu Gly Glu Ser Ala Thr Glu
 245 250 255
 Ser Arg Phe Val Tyr Glu Asn Asn Val Phe Asn Gly Val Gln Leu Val
 260 265 270
 Phe Asn Gly Gly Pro Leu Ala Ser Glu Pro Met Gln Gly Ile Ile Val
 275 280 285
 Arg Leu Lys Lys Ala Glu Lys Arg Glu Val Asp Glu Asp Lys Ile Val
 290 295 300
 Asn Pro Gly Lys Ile Ile Thr Gln Thr Arg Asp Leu Ile Tyr Lys Arg
 305 310 315 320
 Phe Leu Gln Lys Ser Pro Arg Leu Tyr Leu Ala Met Tyr Thr Cys Glu
 325 330 335
 Ile Gln Ala Ala Ala Glu Val Leu Gly Lys Val Tyr Ala Val Val Gln
 340 345 350
 Arg Arg Glu Gly Ser Ile Ile Ser Glu Glu Met Lys Glu Gly Thr Pro
 355 360 365
 Phe Phe Thr Ile Val Ala Arg Ile Pro Val Ile Glu Ala Phe Gly Phe
 370 375 380
 Ser Glu Asp Ile Arg Lys Lys Thr Ser Gly Ala Ala Ser Pro Gln Leu
 385 390 395 400
 Val Phe Asp Gly Tyr Asp Met Leu Asp Ile Asp Pro Phe Trp Val Pro
 405 410 415
 His Thr Glu Glu Glu Leu Glu Glu Leu Gly Glu Phe Ala Glu Arg Glu
 420 425 430
 Asn Val Ala Arg Arg Tyr Met Asn Asn Ile Arg Arg Arg Lys Gly Leu
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 Lys Arg Asp
 465

<210> 70

<211> 1340

<212> DNA

<213> *Candida albicans*

<400> 70

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cctaaatgtc aaaacttagt tggatctggg gttgttatcc acgttccttc cttcttttgc 240
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1340

<210> 71

<211> 428

<212> PRT

<213> *Candida albicans*

<400> 71

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      20              25              30

Gln Gly Gly Asn Asn Ala Gly His Thr Ile Val Val Gly Lys Val Lys
      35              40              45

Tyr Asp Phe His Met Leu Pro Ser Gly Leu Val Asn Pro Lys Cys Gln
      50              55              60

Asn Leu Val Gly Ser Gly Val Val Ile His Val Pro Ser Phe Phe Ala

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65	70	75	80
Glu Leu Glu Asn Leu Glu Ala Lys Gly Leu Asp Cys Arg Asp Arg Leu	85	90	95
Phe Val Ser Ser Arg Ala His Leu Val Phe Asp Phe His Gln Arg Thr	100	105	110
Asp Lys Leu Lys Glu Ala Glu Leu Ser Thr Asn Lys Lys Ser Ile Gly	115	120	125
Thr Thr Gly Lys Gly Ile Gly Pro Thr Tyr Ser Thr Lys Ala Ser Arg	130	135	140
Ser Gly Ile Arg Val His His Leu Val Asn Pro Asp Pro Glu Ala Trp	145	150	155
Glu Glu Phe Lys Thr Arg Tyr Leu Arg Leu Val Glu Ser Arg Gln Lys	165	170	175
Arg Tyr Gly Glu Phe Glu Tyr Asp Pro Lys Glu Glu Leu Ala Arg Phe	180	185	190
Glu Lys Tyr Arg Glu Thr Leu Arg Pro Phe Val Val Asp Ser Val Asn	195	200	205
Phe Met His Glu Ala Ile Ala Ala Asn Lys Lys Ile Leu Val Glu Gly	210	215	220
Ala Asn Ala Leu Met Leu Asp Ile Asp Phe Gly Thr Tyr Pro Tyr Val	225	230	235
Thr Ser Ser Ser Thr Gly Ile Gly Gly Val Leu Thr Gly Leu Gly Ile	245	250	255
Pro Pro Arg Thr Ile Arg Asn Val Tyr Gly Val Val Lys Ala Tyr Thr	260	265	270
Thr Arg Val Gly Glu Gly Pro Phe Pro Thr Glu Gln Leu Asn Lys Val	275	280	285
Gly Glu Thr Leu Gln Asp Val Gly Ala Glu Tyr Gly Val Thr Thr Gly	290	295	300
Arg Lys Arg Arg Cys Gly Trp Leu Asp Leu Val Val Leu Lys Tyr Ser	305	310	315
Asn Ser Ile Asn Gly Tyr Thr Ser Leu Asn Ile Thr Lys Leu Asp Val			320

<400> 72						
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ataacggcat	taacggcagc	aacttcaa	gatgctgggtg	ctactcaaga	ttcattgaat	300
aaaatatatg	gtattttctta	tgattcaatg	aatactgggtg	ctgggggtatt	atttatattt	360
attggatggt	catgtatgtt	tttcgcacca	gcttcttc	tatatggacg	aagaataact	420
tatattattt	gtttattggc	aggaacttta	ggttggtgat	ggtttgctct	ttctaaaaga	480
actgccgata	ctatttggtc	acaagcattt	gtggggatga	gtgaagcttg	tgctgaagct	540
caagttcaac	aatcattaac	tgattttattt	ttggctcatg	aattgggtac	agcattaaca	600
atttatattt	ctgctacttc	aataggtact	ttattgggtc	ctttgattgc	tcaagatatt	660
gctcaagctc	aaactttccg	gtgggtcggg	tggtgggggtg	ccatttatatg	tggtgccact	720
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gtattagaat	ctgaaaatgt	tactcaaatt	ccagacccat	cagaagaaaa	gaaacaagat	840
aaccacctta	caaataatat	cattcctcac	gagaagaaaa	attcaatgga	acaagaatta	900
tctcatgaat	atatcactgc	aaacaataat	gaacatgacg	ttgttccaat	tgatcctgaa	960
actttaaatg	aaaagaaaaa	atcttatttg	caaagaatag	caatcattac	accagcacct	1020
tattttacaag	gttttaggatt	taaacaatat	ttagaacggt	tcattattta	tttcaaaatt	1080
ttcacattac	cagcagtttg	gttttccgga	ttattatggg	ggttacaaga	tacttatatg	1140
acattttttt	taactactca	agacacgtat	ttttataatc	caccatggaa	taaatcaa	1200
gctggtgtag	caattatgaa	tgtagctaca	ttaattgggtg	ctgttatttg	atgcattggt	1260

tctgggttat tttctgatta tcatgttatt tggttagcta aacggaataa tgggataatg 1320
 gaagctgaat atcgattata tttattagtt atcactttaa tcatttcacc cgtaggggta 1380
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 ggtttcattg ggtttggtg gggatcaatt ggtgatactt caatgtctta ttaaatggat 1500
 gcttatcctg atattgtcat tcaaggaatg gtgggagtaa gtattattaa taatactttg 1560
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 tatattgcct tgtcaattat tgattttgct accatagcat tggttttccc ctttttatat 1680
 tatggtaaaa catttagaag gaaaactaaa agactttatg tttcaatggg tgaattgact 1740
 caagggatgg gataagagag tgagtggtaa aagaatttta ttaatgatac atttattatt 1800
 agaattacta ctatggaaat ccgagtctgt gtttttttta gaagtatatt ttagacgtat 1860
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 gcattaatat atataaataa aaaaact 1947

<210> 73

<211> 584

<212> PRT

<213> Candida albicans

<400> 73

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Ile Pro Gly Thr Thr Asn Ile Leu Thr Gly Lys Thr Thr Ile Asp Glu
 20 25 30

Ser Ser Ser Ile Thr Thr Gln Lys Ser Leu Lys Arg Asp Pro Lys Thr
 35 40 45

Gly Leu Val Leu Met Pro Gln Pro Thr Ser Ser Pro Asn Asp Pro Leu
 50 55 60

Asn Trp Ser Pro Phe Arg Lys Phe Ala Gln Leu Thr Leu Leu Ser Phe
 65 70 75 80

Ile Thr Ala Leu Thr Ala Ala Thr Ser Asn Asp Ala Gly Ala Thr Gln
 85 90 95

Asp Ser Leu Asn Lys Ile Tyr Gly Ile Ser Tyr Asp Ser Met Asn Thr
 100 105 110

Gly Ala Gly Val Leu Phe Ile Phe Ile Gly Trp Ser Cys Met Phe Phe
 115 120 125

Ala Pro Ala Ser Ser Leu Tyr Gly Arg Arg Ile Thr Tyr Ile Ile Cys
 130 135 140

Leu Leu Ala Gly Thr Leu Gly Cys Val Trp Phe Ala Leu Ser Lys Arg
 145 150 155 160

Thr Ala Asp Thr Ile Trp Ser Gln Ala Phe Val Gly Met Ser Glu Ala
 165 170 175
 Cys Ala Glu Ala Gln Val Gln Gln Ser Leu Thr Asp Leu Phe Leu Ala
 180 185 190
 His Glu Leu Gly Thr Ala Leu Thr Ile Tyr Ile Ser Ala Thr Ser Ile
 195 200 205
 Gly Thr Leu Leu Gly Pro Leu Ile Ala Gln Asp Ile Ala Gln Ala Gln
 210 215 220
 Thr Phe Arg Trp Val Gly Trp Trp Gly Ala Ile Ile Cys Gly Ala Thr
 225 230 235 240
 Leu Ile Val Ile Ile Phe Gly Cys Glu Glu Thr Val Phe Asp Arg Gln
 245 250 255
 Leu Tyr Thr Lys Val Leu Glu Ser Glu Asn Val Thr Gln Ile Pro Asp
 260 265 270
 Pro Ser Glu Glu Lys Lys Gln Asp Asn Pro Leu Thr Asn Asn Ile Ile
 275 280 285
 Pro His Glu Lys Lys Asn Ser Met Glu Gln Glu Leu Ser His Glu Tyr
 290 295 300
 Ile Thr Ala Asn Asn Asn Glu His Asp Val Val Pro Ile Asp Pro Glu
 305 310 315 320
 Thr Leu Asn Glu Lys Lys Lys Ser Tyr Trp Gln Arg Ile Ala Ile Ile
 325 330 335
 Thr Pro Ala Pro Tyr Leu Gln Gly Leu Gly Phe Lys Gln Tyr Leu Glu
 340 345 350
 Arg Phe Ile Ile Tyr Phe Lys Ile Phe Thr Leu Pro Ala Val Trp Phe
 355 360 365
 Ser Gly Leu Leu Trp Gly Leu Gln Asp Thr Tyr Met Thr Phe Phe Leu
 370 375 380
 Thr Thr Gln Asp Thr Tyr Phe Tyr Asn Pro Pro Trp Asn Lys Ser Asn
 385 390 395 400
 Ala Gly Val Ala Ile Met Asn Val Ala Thr Leu Ile Gly Ala Val Ile
 405 410 415

Gly Cys Ile Val Ser Gly Leu Phe Ser Asp Tyr His Val Ile Trp Leu
 420 425 430
 Ala Lys Arg Asn Asn Gly Ile Met Glu Ala Glu Tyr Arg Leu Tyr Leu
 435 440 445
 Leu Val Ile Thr Leu Ile Ile Ser Pro Val Gly Leu Ile Met Phe Gly
 450 455 460
 Val Gly Ala Ala Arg Glu Trp Pro Trp Gln Val Ile Tyr Val Gly Leu
 465 470 475 480
 Gly Phe Ile Gly Phe Gly Trp Gly Ser Ile Gly Asp Thr Ser Met Ser
 485 490 495
 Tyr Leu Met Asp Ala Tyr Pro Asp Ile Val Ile Gln Gly Met Val Gly
 500 505 510
 Val Ser Ile Ile Asn Asn Thr Leu Ala Cys Ile Phe Thr Phe Ala Cys
 515 520 525
 Ser Tyr Trp Leu Asp Gly Ser Gly Thr Gln Asn Thr Tyr Ile Ala Leu
 530 535 540
 Ser Ile Ile Asp Phe Ala Thr Ile Ala Leu Val Phe Pro Phe Leu Tyr
 545 550 555 560
 Tyr Gly Lys Thr Phe Arg Arg Lys Thr Lys Arg Leu Tyr Val Ser Met
 565 570 575
 Val Glu Leu Thr Gln Gly Met Gly
 580

<210> 74

<211> 1018

<212> DNA

<213> Candida albicans

<400> 74

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 tcggtgttgt tgaatgcgct tcaatttgca ttcaagttaa ttgcccacaa tatcagaaga 180
 gctgagttgg tcaaccttat tgggtgtttct ggctctgcca actctaccgg tgatgttcag 240
 aagaaattgg atgtgattgg tgatgagatc tttatcaatg ccatgagatc ttccaacaac 300
 gtcaagggtt tgggtttctga agagcaagaa gaccttattg tgttcccagg tgggtggcaca 360
 tatgctgttt gtactgatcc aattgatggg tcgtccaata tcgatgctgg tgtttctgtt 420

ggtacgattt ttggtgtgta caagttgcaa gaggggtcta ctggtggcat cagcgatgtc 480
 ttgcgtcctg gtaaggagat ggtcgctgcg gggtacacca tgtacgggtgc atctgccccat 540
 ttggcattga ctacaggtca cgggtgtcaat ctttttactt tggatactca gttgggtgaa 600
 tttatcttga cccatccaaa cttgaagttg ccagatacta agaacatcta ctcgttgaat 660
 gaagggtact cgaacaaatt cccagaatac gttcaagatt atctgaagga cattaataaag 720
 gaagggtaca gtttgagata cattggactg atggttgctg atgtccatcg tactcttttg 780
 tatggtggta tttttgctta ccctacatta aagttgagag tgttgatga atgtttcccc 840
 atggccttgt tgatggaaca agcaggcggg tctgctgtca ccatcaaggg tgagaggatc 900
 ttggatatct tgccaaaagg tatacacgac aagagttcta ttgtgttggg atccaagggt 960
 gaagttgaaa agtatttaaa gcatgtacca aaatagatta tgtagaaaat ttatgaac 1018

<210> 75

<211> 331

<212> PRT

<213> Candida albicans

<400> 75

Met Ser Gly Pro Val Asn Ser Val Ser Lys Gln Met Asn Val Asp Thr
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Asp Ile Ile Thr Leu Thr Arg Phe Ile Leu Gln Glu Gln Gln Thr Val
 20 25 30

Ala Pro Thr Ala Thr Gly Glu Leu Ser Leu Leu Leu Asn Ala Leu Gln
 35 40 45

Phe Ala Phe Lys Phe Ile Ala His Asn Ile Arg Arg Ala Glu Leu Val
 50 55 60

Asn Leu Ile Gly Val Ser Gly Ser Ala Asn Ser Thr Gly Asp Val Gln
 65 70 75 80

Lys Lys Leu Asp Val Ile Gly Asp Glu Ile Phe Ile Asn Ala Met Arg
 85 90 95

Ser Ser Asn Asn Val Lys Val Leu Val Ser Glu Glu Gln Glu Asp Leu
 100 105 110

Ile Val Phe Pro Gly Gly Gly Thr Tyr Ala Val Cys Thr Asp Pro Ile
 115 120 125

Asp Gly Ser Ser Asn Ile Asp Ala Gly Val Ser Val Gly Thr Ile Phe
 130 135 140

Gly Val Tyr Lys Leu Gln Glu Gly Ser Thr Gly Gly Ile Ser Asp Val
 145 150 155 160

Leu Arg Pro Gly Lys Glu Met Val Ala Ala Gly Tyr Thr Met Tyr Gly

165 170 175
 Ala Ser Ala His Leu Ala Leu Thr Thr Gly His Gly Val Asn Leu Phe
 180 185 190
 Thr Leu Asp Thr Gln Leu Gly Glu Phe Ile Leu Thr His Pro Asn Leu
 195 200 205
 Lys Leu Pro Asp Thr Lys Asn Ile Tyr Ser Leu Asn Glu Gly Tyr Ser
 210 215 220
 Asn Lys Phe Pro Glu Tyr Val Gln Asp Tyr Ser Lys Asp Ile Lys Lys
 225 230 235 240
 Glu Gly Tyr Ser Leu Arg Tyr Ile Gly Ser Met Val Ala Asp Val His
 245 250 255
 Arg Thr Leu Leu Tyr Gly Gly Ile Phe Ala Tyr Pro Thr Leu Lys Leu
 260 265 270
 Arg Val Leu Tyr Glu Cys Phe Pro Met Ala Leu Leu Met Glu Gln Ala
 275 280 285
 Gly Gly Ser Ala Val Thr Ile Lys Gly Glu Arg Ile Leu Asp Ile Leu
 290 295 300
 Pro Lys Gly Ile His Asp Lys Ser Ser Ile Val Leu Gly Ser Lys Gly
 305 310 315 320
 Glu Val Glu Lys Tyr Leu Lys His Val Pro Lys
 325 330

 <210> 76
 <211> 1686
 <212> DNA
 <213> Candida albicans

 <400> 76
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 aattcgatgc gatgcaatga agtttaataa aatttttttt tttctttatt tcttttaatc 180
 aacccatcaa tcattaaatt gaatcaatac ctaccattaa catacttcta tatacatata 240
 tatatataac aaaatatcat ggggaagata acaactagt atactaaaac aaaacaacgt 300
 cataatccat tattaaga ttttcatcc caagggtgga atttaagaac cgttccaaga 360
 tcatcatcat catcatcatc acaaaagaag aaatcatcaa agaaacaaag acataacgat 420
 gaagacgacg aagaaaatgg tggcggtgaa ggatttttag atgcttctag ttcaagaaag 480
 attttacaat tggcaaaaaga acaacaagat gaacttgaac aagaagatga aatacaaaat 540

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aaaccttcat ttgctcaatc atttaaaaat caacaaatag atagtgaaga agaagaagag 600
gaagatgagt attcagattt tgaagaagaa gaagaagttg aagagatagt atatgatgaa 660
gaagatgcag aagttgatcc caaagatgca gaattattta ataaatattt ccaatccaac 720
ggtgaagcta ataataatga tgatgataat tcatttcaac caacaataaa tttagctgat 780
aaaatcttag ccaaaattca agaaaaagaa tcccaacaac aacaacaaca acaaagctct 840
ccagataata gtaatgaaga tgccgtattg ttaccaccaa aagtcatttt agcttatgaa 900
aaaattgggtc aaattttatc aacttatact catgggaaat tacctaaatt atttaaaatt 960
ttaccaagtt taaaaaattg gcaagatgta ttatacgtga caaatccaaa tagttggact 1020
cctcatgccca catatgaagc aactaaatta tttgtgtcga atttatcaag taatgaagct 1080
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gatcattcat taaattatca ttttatcga gcattaaaaa aatcattata taaaccagga 1200
gcttttttca aagggttctt gttaccttta gtcatgggtt attgttctgt acgtgaagcc 1260
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ttaactcaat tattaactag agattttaat cctgctacaa cggttttcat tagagtttta 1380
attgaaaaaa aatatgcttt accttatcaa actttagatg aattagtatt ttatttcattg 1440
agatttagaa atgctactat taatcaagat gaaaatatgg aaaatatgga tattgatcaa 1500
gaaaaaacca ccaaagtcaa taatgggtcct caattaccag tggatggca taaagcattc 1560
ttatcatttg ctactcgtta taaaaatgat cttactgatg atcaaaaaga tttcttatta 1620
gaaacagtaa gacaaagatt tcacacctta attggctcctg aaattcgtag agaattacta 1680
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1686

<210> 77

<211> 475

<212> PRT

<213> Candida albicans

<400> 77

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Met Gly Lys Ile Thr Thr Ser Asp Thr Lys Thr Lys Gln Arg His Asn
  1                      5                      10                      15

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Pro Leu Leu Lys Asp Ile Ser Ser Gln Gly Gly Asn Leu Arg Thr Val
      20                      25                      30

```

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Pro Arg Ser Ser Ser Ser Ser Ser Ser Gln Lys Lys Lys Ser Ser Lys
      35                      40                      45

```

```

Lys Gln Arg His Asn Asp Glu Asp Asp Glu Glu Asn Gly Gly Gly Glu
      50                      55                      60

```

```

Gly Phe Leu Asp Ala Ser Ser Ser Arg Lys Ile Leu Gln Leu Ala Lys
      65                      70                      75                      80

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```

Glu Gln Gln Asp Glu Leu Glu Gln Glu Asp Glu Ile Gln Asn Lys Pro
      85                      90                      95

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Ser Phe Ala Gln Ser Phe Lys Asn Gln Gln Ile Asp Ser Glu Glu Glu
      100                      105                      110

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Glu Glu Glu Asp Glu Tyr Ser Asp Phe Glu Glu Glu Glu Glu Val Glu
 115 120 125

Glu Ile Val Tyr Asp Glu Glu Asp Ala Glu Val Asp Pro Lys Asp Ala
 130 135 140

Glu Leu Phe Asn Lys Tyr Phe Gln Ser Asn Gly Glu Ala Asn Asn Asn
 145 150 155 160

Asp Asp Asp Asn Ser Phe Gln Pro Thr Ile Asn Leu Ala Asp Lys Ile
 165 170 175

Leu Ala Lys Ile Gln Glu Lys Glu Ser Gln Gln Gln Gln Gln Gln Gln
 180 185 190

Ser Ser Pro Asp Asn Ser Asn Glu Asp Ala Val Leu Leu Pro Pro Lys
 195 200 205

Val Ile Leu Ala Tyr Glu Lys Ile Gly Gln Ile Leu Ser Thr Tyr Thr
 210 215 220

His Gly Lys Leu Pro Lys Leu Phe Lys Ile Leu Pro Ser Leu Lys Asn
 225 230 235 240

Trp Gln Asp Val Leu Tyr Val Thr Asn Pro Asn Ser Trp Thr Pro His
 245 250 255

Ala Thr Tyr Glu Ala Thr Lys Leu Phe Val Ser Asn Leu Ser Ser Asn
 260 265 270

Glu Ala Thr Val Phe Ile Glu Thr Ile Leu Leu Pro Arg Phe Arg Asp
 275 280 285

Ser Ile Glu Asn Ser Asp Asp His Ser Leu Asn Tyr His Ile Tyr Arg
 290 295 300

Ala Leu Lys Lys Ser Leu Tyr Lys Pro Gly Ala Phe Phe Lys Gly Phe
 305 310 315 320

Leu Leu Pro Leu Val Asp Gly Tyr Cys Ser Val Arg Glu Ala Thr Ile
 325 330 335

Ala Ala Ser Val Leu Thr Lys Val Ser Val Pro Val Leu His Ser Ser
 340 345 350

Val Ala Leu Thr Gln Leu Leu Thr Arg Asp Phe Asn Pro Ala Thr Thr
 355 360 365

Val Phe Ile Arg Val Leu Ile Glu Lys Lys Tyr Ala Leu Pro Tyr Gln
 370 375 380

Thr Leu Asp Glu Leu Val Phe Tyr Phe Met Arg Phe Arg Asn Ala Thr
 385 390 395 400

Ile Asn Gln Asp Glu Asn Met Glu Asn Met Asp Ile Asp Gln Glu Lys
 405 410 415

Thr Thr Lys Val Asn Asn Gly Pro Gln Leu Pro Val Val Trp His Lys
 420 425 430

Ala Phe Leu Ser Phe Ala Thr Arg Tyr Lys Asn Asp Leu Thr Asp Asp
 435 440 445

Gln Lys Asp Phe Leu Leu Glu Thr Val Arg Gln Arg Phe His Pro Leu
 450 455 460

Ile Gly Pro Glu Ile Arg Arg Glu Leu Leu Ser
 465 470 475

<210> 78

<211> 1519

<212> DNA

<213> Candida albicans

<400> 78

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 ctccgccccct tcctttttcat atactatctc ccttccttct tccttctcct tttatttttt 180
 caattattac aatcttatgt catttaaagg attcaaaaag ggtgtcctta gggccccaca 240
 gacaatgcgt cagaaattca acatgggaga aatcacccaa gatgctgttt atctcgatgc 300
 tgaaagaaga ttcaaagaaa tcgaaacgga aacaaaaaag ttgagtgaag aatccaagaa 360
 atattttcaat gctgtcaatg ggatgttaga tgaacaaatt gattttgcca aagccgtggc 420
 tgagatttat aaaccaatca gtggtagatt atcggacccc agtgctacgg taccagaaga 480
 taaccacaaa ggtattgaag catcggaact gtaccaagca gtggttaaag atctcaaaga 540
 taccttaaaa cccgatttgg aattgattga aaaaagaatt gttgaaccag cacaagaatt 600
 attgaagatt atacaagcta taaggaaaaat gtcagtgaag agagaccata aacaattgga 660
 tttggatcgt cataagagaa atttttctaa atatgaactg aagaaagaaa gaactgttaa 720
 agatgaagaa aaaatgttca gtgctcaagc agaagtagaa attgctcaac aagagtacga 780
 ttattataat gatttggtta agaatgaatt gccagttttg tttcaaattgc aaagtgtatt 840
 tatcaaacca ttgtttgttt cattctatta catgcagttg aatattttct acacattata 900
 cactagaatg gaagagttga aaattccata ttttgatttg tctactgata ttgtcgaagc 960
 ttatactgcc aagaagggga acattgagga acaaaccgat gctattggaa tcaactatctt 1020
 caaagtcggg catgccaaat ccaaattgga agccactaaa agaagacatg ctgctatgaa 1080
 tagtccacct cctaccggtg ccagctctat tgcacttaca ggtactggtg gtgaattacc 1140
 tgcatactcc ccaggagggtt acaaccaacc atatggtgat agcaagtatc aaccaccatc 1200

ttctccagca acataccaat ctccagtagt agcagccact gctcaatctc cagctactta 1260
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 tccaccacca caagttggta gtggccttcc aacatgcacg gctttatacg attatactgc 1380
 acaagcccag ggtgacttga ctttccctgc aggagctggt attgaaatta tacaaagaac 1440
 cgaagatgcc aacggatggt ggactggtaa atacaatggt caaaccggtg tggtccctgg 1500
 taattatgtg caattatag 1519

<210> 79

<211> 440

<212> PRT

<213> Candida albicans

<400> 79

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		20						25					30		
Leu	Asp	Ala	Glu	Arg	Arg	Phe	Lys	Glu	Ile	Glu	Thr	Glu	Thr	Lys	Lys
	35						40					45			
Leu	Ser	Glu	Glu	Ser	Lys	Lys	Tyr	Phe	Asn	Ala	Val	Asn	Gly	Met	Leu
50					55						60				
Asp	Glu	Gln	Ile	Asp	Phe	Ala	Lys	Ala	Val	Ala	Glu	Ile	Tyr	Lys	Pro
65				70					75					80	
Ile	Ser	Gly	Arg	Leu	Ser	Asp	Pro	Ser	Ala	Thr	Val	Pro	Glu	Asp	Asn
		85						90					95		
Pro	Gln	Gly	Ile	Glu	Ala	Ser	Glu	Ser	Tyr	Gln	Ala	Val	Val	Lys	Asp
	100						105						110		
Leu	Lys	Asp	Thr	Leu	Lys	Pro	Asp	Leu	Glu	Leu	Ile	Glu	Lys	Arg	Ile
	115					120					125				
Val	Glu	Pro	Ala	Gln	Glu	Leu	Leu	Lys	Ile	Ile	Gln	Ala	Ile	Arg	Lys
130					135						140				
Met	Ser	Val	Lys	Arg	Asp	His	Lys	Gln	Leu	Asp	Leu	Asp	Arg	His	Lys
145				150					155					160	
Arg	Asn	Phe	Ser	Lys	Tyr	Glu	Ser	Lys	Lys	Glu	Arg	Thr	Val	Lys	Asp
		165						170					175		
Glu	Glu	Lys	Met	Phe	Ser	Ala	Gln	Ala	Glu	Val	Glu	Ile	Ala	Gln	Gln
	180						185						190		

Glu Tyr Asp Tyr Tyr Asn Asp Leu Leu Lys Asn Glu Leu Pro Val Leu
 195 200 205
 Phe Gln Met Gln Ser Asp Phe Ile Lys Pro Leu Phe Val Ser Phe Tyr
 210 215 220
 Tyr Met Gln Leu Asn Ile Phe Tyr Thr Leu Tyr Thr Arg Met Glu Glu
 225 230 235 240
 Leu Lys Ile Pro Tyr Phe Asp Leu Ser Thr Asp Ile Val Glu Ala Tyr
 245 250 255
 Thr Ala Lys Lys Gly Asn Ile Glu Glu Gln Thr Asp Ala Ile Gly Ile
 260 265 270
 Thr His Phe Lys Val Gly His Ala Lys Ser Lys Leu Glu Ala Thr Lys
 275 280 285
 Arg Arg His Ala Ala Met Asn Ser Pro Pro Pro Thr Gly Ala Ser Ser
 290 295 300
 Ile Ala Ser Thr Gly Thr Gly Gly Glu Leu Pro Ala Tyr Ser Pro Gly
 305 310 315 320
 Gly Tyr Asn Gln Pro Tyr Gly Asp Ser Lys Tyr Gln Pro Pro Ser Ser
 325 330 335
 Pro Ala Thr Tyr Gln Ser Pro Val Val Ala Ala Thr Ala Gln Ser Pro
 340 345 350
 Ala Thr Tyr Gln Ser Pro Val Ala Thr Gly Gln Pro Pro Ser Tyr Leu
 355 360 365
 Pro Gln Thr Pro Ala Ser Ala Pro Pro Pro Gln Val Gly Ser Gly Leu
 370 375 380
 Pro Thr Cys Thr Ala Leu Tyr Asp Tyr Thr Ala Gln Ala Gln Gly Asp
 385 390 395 400
 Leu Thr Phe Pro Ala Gly Ala Val Ile Glu Ile Ile Gln Arg Thr Glu
 405 410 415
 Asp Ala Asn Gly Trp Trp Thr Gly Lys Tyr Asn Gly Gln Thr Gly Val
 420 425 430
 Phe Pro Gly Asn Tyr Val Gln Leu
 435 440

<210> 80
 <211> 861
 <212> DNA
 <213> *Candida albicans*

<400> 80
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 ggtcccgtca aatcaatcaa tatgccaaag gatcgtatat tgaaaacaca ccaggggtat 180
 ggatttgctg aatttaaaaa ctacgcagat gccaaatata ctatggaaat actacgagga 240
 ataagacttt atggaaaagc attgaaattg aaacgaattg atgccaagtc tcagtcatca 300
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 gagcggaaat tggctgaaag tgccaaaaag aataatttgt tggtaacgaa aacttctaag 720
 gcaggtagca cgaagggaaa taaaaggaag aataaaccac ataaagtac caaacgtga 780
 gacaatgagt tagctcccc tttcaaaaata agtagagtat caccatagtt tatgaaacaa 840
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 861

<210> 81
 <211> 1641
 <212> DNA
 <213> *Candida albicans*

<400> 81
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<210> 82

<211> 546

<212> PRT

<213> *Candida albicans*

<400> 82

Met Ser Gln Asp Asn Val Ser Ser Thr Ser Thr Ala Glu Ala Val Asn
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Asn Glu Ile Lys Val Lys Asp Glu Phe Pro Gln Glu Glu Gln Ala His
 20 25 30

Thr Ser Leu Glu Asp Lys Pro Val Ser Ala Tyr Ile Gly Ile Ile Ile
 35 40 45

Met Cys Phe Leu Ile Ala Phe Gly Gly Phe Val Phe Gly Phe Asp Thr
 50 55 60

Gly Thr Ile Ser Gly Phe Ile Asn Met Ser Asp Phe Leu Glu Arg Phe
 65 70 75 80

Gly Gly Thr Lys Ala Asp Gly Thr Leu Tyr Phe Ser Asn Val Arg Thr
 85 90 95

Gly Val Met Ile Gly Leu Phe Asn Ala Gly Gly Ala Ile Gly Ala Leu
 100 105 110

Phe Leu Ser Lys Val Gly Asp Met Tyr Gly Arg Arg Val Gly Ile Met
 115 120 125

Thr Ala Met Ile Val Tyr Ile Val Gly Ile Ile Val Gln Ile Ala Ser
 130 135 140

Gln His Ala Trp Tyr Gln Val Met Ile Gly Arg Ile Ile Thr Gly Leu
 145 150 155 160

Ala Val Gly Met Leu Ser Val Leu Cys Pro Leu Phe Ile Ser Glu Val

165 170 175
 Ser Pro Lys His Leu Arg Gly Thr Leu Val Cys Cys Phe Gln Leu Met
 180 185 190
 Ile Thr Leu Gly Ile Phe Leu Gly Tyr Cys Thr Thr Tyr Gly Thr Lys
 195 200 205
 Ser Tyr Ser Asp Ser Arg Gln Trp Arg Ile Pro Leu Gly Leu Cys Phe
 210 215 220
 Ala Trp Ala Leu Cys Leu Val Ala Gly Met Val Arg Met Pro Glu Ser
 225 230 235 240
 Pro Arg Tyr Leu Val Gly Lys Asp Arg Ile Glu Asp Ala Lys Met Ser
 245 250 255
 Leu Ala Lys Thr Asn Lys Val Ser Pro Glu Asp Pro Ala Leu Tyr Arg
 260 265 270
 Glu Leu Gln Leu Ile Gln Ala Gly Val Glu Arg Glu Arg Leu Ala Gly
 275 280 285
 Lys Ala Ser Trp Gly Thr Leu Phe Asn Gly Lys Pro Arg Ile Phe Glu
 290 295 300
 Arg Val Ile Val Gly Val Met Leu Gln Ala Leu Gln Gln Leu Thr Gly
 305 310 315 320
 Asp Asn Tyr Phe Phe Tyr Tyr Ser Thr Thr Ile Phe Lys Ser Val Gly
 325 330 335
 Met Asn Asp Ser Phe Glu Thr Ser Ile Ile Ile Gly Val Ile Asn Phe
 340 345 350
 Ala Ser Thr Phe Val Gly Ile Tyr Ala Ile Glu Arg Met Gly Arg Arg
 355 360 365
 Leu Cys Leu Leu Thr Gly Ser Val Ala Met Ser Ile Cys Phe Leu Ile
 370 375 380
 Tyr Ser Leu Val Gly Thr Gln His Leu Tyr Ile Asp Lys Pro Gly Gly
 385 390 395 400
 Ala Ser Arg Lys Pro Asp Gly Asp Ala Met Ile Phe Met Thr Pro Leu
 405 410 415
 Tyr Val Ile Phe Ser Pro Ser Thr Trp Ala Gly Gly Val Tyr Ser Ile

101

tacttagcat tgacttacga ccacagagta gttgacggtc gtgaagctgt tattttctta 960
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<210> 84

<211> 337

<212> PRT

<213> Candida albicans

<400> 84

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 Ala Thr Val Glu Val Gly Gln Glu Ile Ile Lys Met Glu Glu Gly Asp
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 Ala Pro Ala Gly Gly Ala Ser Ala Ser Glu Ala Pro Ala Lys Lys Glu
 35 40 45
 Glu Ala Pro Glu Lys Ala Lys Glu Glu Ser Ala Gln Ala Ala Ala Pro
 50 55 60
 Lys Lys Glu Glu Thr Lys Lys Glu Glu Pro Lys Lys Glu Ser Lys Pro
 65 70 75 80
 Ala Pro Lys Lys Glu Glu Ser Lys Lys Ser Thr Gln Ser Thr Thr Ser
 85 90 95
 Ala Pro Thr Phe Thr Asn Phe Ser Arg Asn Glu Glu Arg Val Lys Met
 100 105 110
 Asn Arg Met Arg Leu Arg Ile Ala Glu Arg Leu Lys Glu Ser Gln Asn
 115 120 125
 Thr Ala Ala Ser Leu Thr Thr Phe Asn Glu Val Asp Met Ser Asn Leu
 130 135 140
 Met Asp Phe Arg Lys Lys Tyr Lys Asp Glu Phe Ile Glu Lys Thr Gly
 145 150 155 160
 Ile Lys Leu Gly Phe Met Gly Ala Phe Ser Lys Ala Ser Ala Leu Ala
 165 170 175
 Leu Lys Glu Ile Pro Ala Val Asn Ala Ala Ile Glu Asn Asn Asp Thr
 180 185 190
 Leu Val Phe Lys Asp Tyr Ala Asp Ile Ser Ile Ala Val Ala Thr Pro
 195 200 205

Lys Gly Leu Val Thr Pro Val Val Arg Asn Ala Glu Ser Leu Ser Ile
 210 215 220
 Leu Gly Ile Glu Lys Glu Ile Ser Asn Leu Gly Lys Lys Ala Arg Asp
 225 230 235 240
 Gly Lys Leu Thr Leu Glu Asp Met Thr Gly Gly Thr Phe Thr Ile Ser
 245 250 255
 Asn Gly Gly Val Phe Gly Ser Leu Tyr Gly Thr Pro Ile Ile Asn Met
 260 265 270
 Pro Gln Thr Ala Val Leu Gly Leu His Gly Val Lys Glu Arg Pro Val
 275 280 285
 Thr Val Asn Gly Gln Ile Val Ser Arg Pro Met Met Tyr Leu Ala Leu
 290 295 300
 Thr Tyr Asp His Arg Val Val Asp Gly Arg Glu Ala Val Ile Phe Leu
 305 310 315 320
 Arg Thr Ile Lys Glu Leu Ile Glu Asp Pro Arg Lys Met Leu Leu Leu
 325 330 335
 Glu

<210> 85
 <211> 1806
 <212> DNA
 <213> Candida albicans

<400> 85
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 cttttttacac tgctgtgata tcggttattg gttctgcccgg tttgatcggg tacaaaattt 240
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 tggataccac cttgtataat gttgttattg tctccccaag aaactatttc cttttcaccc 420
 cattgttacc atctgttcct accggtactg ttgaattgag atctattatt gaacctgtca 480
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 ctggtaaaga tacttcctct tctaaatcaa ctggtgccga atacactggg gttgaagaaa 660
 tcaactaccac cttgaattat gactatttag ttggtggtgt tgggtgctcaa ccatctactt 720
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 ccgatgaatt gaaagtctcc ttggtggaag ctttaccaaa cgttttgaac acattttaaca 1020
 agaaattgat tgactatacc aaagaagttt tcaaagacac taatatcaat ttgatgacta 1080
 ataccatgat caaaaaagtc aatgataaaa gtttgattgc aaaccataaa aaccctgacg 1140
 gatctactga gtctattgaa attccatatg gtcttttaaat ttggggtact ggtaatgcac 1200
 caagagattt cactcgtgat ttgatcgcaa aagtcgatga acaaaaaaat gccagaagag 1260
 gtttattggt tgatgaaaga ttgaaagttg atgggtactga taacattttt gccttgggtg 1320
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 agccgt 1806

<210> 86

<211> 574

<212> PRT

<213> *Candida albicans*

<400> 86

Met Phe Thr Arg Ser Leu Ile Lys Gly Gly Gly Arg Leu Ala Thr Thr
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Lys Lys Tyr Ser Thr Ser Thr Pro Pro Lys Val Ala Lys Ser Lys Ser
 35 40 45

Ser Thr Ile Gly Lys Ile Phe Arg Tyr Thr Phe Tyr Thr Ala Val Ile
 50 55 60

Ser Val Ile Gly Ser Ala Gly Leu Ile Gly Tyr Lys Ile Tyr Glu Glu
 65 70 75 80

Ser Gln Pro Val Asp Gln Val Lys Gln Thr Pro Leu Phe Pro Asn Gly
 85 90 95

Glu Lys Lys Lys Thr Leu Val Ile Leu Gly Ser Gly Trp Gly Ala Ile
 100 105 110

Ser Leu Leu Lys Asn Leu Asp Thr Thr Leu Tyr Asn Val Val Ile Val
 115 120 125

Ser Pro Arg Asn Tyr Phe Leu Phe Thr Pro Leu Leu Pro Ser Val Pro
 130 135 140

Thr Gly Thr Val Glu Leu Arg Ser Ile Ile Glu Pro Val Arg Ser Val
 145 150 155 160

Thr Arg Arg Cys Pro Gly Gln Val Ile Tyr Leu Glu Ala Glu Ala Thr
 165 170 175

Asn Ile Asn Pro Lys Thr Asn Glu Leu Thr Leu Lys Gln Ser Thr Thr
 180 185 190

Val Val Ser Gly His Ser Gly Lys Asp Thr Ser Ser Ser Lys Ser Thr
 195 200 205

Val Ala Glu Tyr Thr Gly Val Glu Glu Ile Thr Thr Thr Leu Asn Tyr
 210 215 220

Asp Tyr Leu Val Val Gly Val Gly Ala Gln Pro Ser Thr Phe Gly Ile
 225 230 235 240

Pro Gly Val Ala Glu Asn Ser Thr Phe Leu Lys Glu Val Ser Asp Ala
 245 250 255

Ser Ala Ile Arg Arg Lys Leu Met Asp Val Ile Glu Ala Ala Asn Ile
 260 265 270

Leu Pro Lys Asp Asp Pro Glu Arg Lys Arg Leu Leu Ser Ile Val Val
 275 280 285

Cys Gly Gly Gly Pro Thr Gly Val Glu Ala Ala Gly Glu Ile Gln Asp
 290 295 300

Tyr Ile Asp Gln Asp Leu Lys Lys Trp Val Pro Glu Val Ala Asp Glu
 305 310 315 320

Leu Lys Val Ser Leu Val Glu Ala Leu Pro Asn Val Leu Asn Thr Phe
 325 330 335

Asn Lys Lys Leu Ile Asp Tyr Thr Lys Glu Val Phe Lys Asp Thr Asn
 340 345 350

Ile Asn Leu Met Thr Asn Thr Met Ile Lys Lys Val Asn Asp Lys Ser
 355 360 365

Leu Ile Ala Asn His Lys Asn Pro Asp Gly Ser Thr Glu Ser Ile Glu
 370 375 380

Ile Pro Tyr Gly Leu Leu Ile Trp Ala Thr Gly Asn Ala Pro Arg Asp
 385 390 395 400
 Phe Thr Arg Asp Leu Ile Ala Lys Val Asp Glu Gln Lys Asn Ala Arg
 405 410 415
 Arg Gly Leu Leu Val Asp Glu Arg Leu Lys Val Asp Gly Thr Asp Asn
 420 425 430
 Ile Phe Ala Leu Gly Asp Cys Thr Phe Thr Lys Tyr Pro Pro Thr Ala
 435 440 445
 Gln Val Ala Phe Gln Glu Gly Glu Tyr Leu Ala Asn Tyr Phe Asp Lys
 450 455 460
 Leu His Ala Val Glu Ser Leu Lys Tyr Thr Ile Ala Asn Pro Thr Pro
 465 470 475 480
 Lys Asp Asn Val Glu Lys Leu Ser Arg Lys Leu Ala Arg Leu Glu Lys
 485 490 495
 Asn Leu Pro His Phe Ile Tyr Asn Tyr Gln Gly Ser Leu Ala Tyr Ile
 500 505 510
 Gly Ser Glu Lys Ala Val Ala Asp Leu Val Trp Gly Asp Trp Ser Asn
 515 520 525
 Ile Ser Ser Gly Gly Asn Leu Thr Phe Leu Phe Trp Arg Ser Ala Tyr
 530 535 540
 Ile Tyr Met Cys Leu Ser Val Lys Asn Gln Val Leu Val Val Leu Asp
 545 550 555 560
 Trp Ala Lys Val Tyr Phe Phe Gly Arg Asp Cys Ser Lys Glu
 565 570

 <210> 87
 <211> 1137
 <212> DNA
 <213> *Candida albicans*

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 aatagatgtc cgctttgtaa aacagagggtt tttgaaagtg gtctaaaacg tgatccattg 240
 ttagaagaga tcgtcggttag ttatgcctcc cttaggcctc atttattacg attattggag 300

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 caacagttga aacaatggga aatggtgcaa catcaaccgt cgtttggtga tgcagagtgg 1080
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<210> 88

<211> 378

<212> PRT

<213> Candida albicans

<400> 88

Met Asn Leu Lys Asp Ile Thr Asp Pro Ser Asp Phe Lys Thr Thr Lys
 1 5 10 15

Leu Pro Ala Leu Ala Glu Leu Asp Ile Leu Lys Arg Cys Tyr Ile Cys
 20 25 30

Lys Asp Leu Leu Asn Ala Pro Val Arg Thr Gln Cys Asp His Thr Tyr
 35 40 45

Cys Ser Gln Cys Ile Arg Glu Phe Leu Leu Arg Asp Asn Arg Cys Pro
 50 55 60

Leu Cys Lys Thr Glu Val Phe Glu Ser Gly Leu Lys Arg Asp Pro Leu
 65 70 75 80

Leu Glu Glu Ile Val Val Ser Tyr Ala Ser Leu Arg Pro His Leu Leu
 85 90 95

Arg Leu Leu Glu Ile Glu Lys Val Glu Ser Lys Gln Glu Val Asp Arg
 100 105 110

Glu Lys Ser Ala Asn Glu Ser Ala Ser Asn Gly Asn Arg Asn Val Asn
 115 120 125

Asn Asp Val Asp Glu Thr Ala Arg Val Lys Asp Gln Ser Asn Ala Asp
 130 135 140

Glu Leu Gly Glu Glu Lys Gly Gln Ala Gln His Gly Glu Gln Val Asn
 145 150 155 160
 Glu Gln Thr Thr Glu Val Ile Ser Leu Leu Ser Asp Asp Glu Glu Asn
 165 170 175
 Gly Ser Asp Ser Leu Val Lys Cys Pro Ile Cys Phe Glu Arg Met Glu
 180 185 190
 Leu Asp Val Leu Gln Gly Lys His Ile Asp Asp Cys Leu Ser Gly Lys
 195 200 205
 Ser Thr Lys Arg Thr Pro Thr Asp Ile Leu Ser Pro Lys Ala Lys Arg
 210 215 220
 Pro Lys Gln Ile Thr Ser Phe Phe Lys Pro Thr Ile Asp Thr Lys Thr
 225 230 235 240
 Pro Ser Pro Pro Thr Ser Lys Ala Ser Thr Thr Pro Thr Ala Thr Pro
 245 250 255
 Thr Thr Thr Leu Leu Lys Ala Asn Val Ala Ser Pro Ser Pro Val Ala
 260 265 270
 Gln Ser Thr Val His Lys Gly Lys Pro Leu Pro Lys Leu Asp Phe Ser
 275 280 285
 Ser Leu Ser Thr Gln Lys Ile Lys Ala Lys Leu Ser Asp Leu Lys Leu
 290 295 300
 Pro Thr Thr Gly Ser Arg Asn Glu Met Glu Ala Arg Tyr Leu His Tyr
 305 310 315 320
 Tyr Val Ile Tyr Asn Ala Asn Leu Asp Ser Asn His Pro Val Lys Glu
 325 330 335
 Ser Ile Leu Arg Gln Gln Leu Lys Gln Trp Glu Met Val Gln His Gln
 340 345 350
 Pro Ser Phe Gly Asp Ala Glu Trp Lys Gly Ala Glu Thr Gly Asn Trp
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 Lys Glu Leu Ile Ala Arg Ala Arg Ser Asn
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<210> 89

<211> 764

<212> DNA

<213> *Candida albicans*

<400> 89

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<210> 90

<211> 179

<212> PRT

<213> *Candida albicans*

<400> 90

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      20             25             30

Asp Thr Thr Ala Phe Gln Ala Pro Pro Thr Lys Ala Pro Glu Ala Ser
      35             40             45

Met Asp Ser Gly Thr Ile Pro Lys Arg Ser Pro Ala Arg Leu Phe Gln
      50             55             60

Arg Trp Ile Ser Ser Ser Ser Lys Asp Lys Pro Val Tyr Ala Glu
      65             70             75             80

Lys Ala Leu Leu Lys Lys Gln Asn Ile Ala Pro Glu Pro Ile Lys Ile
      85             90             95

Thr Lys Gln Gln Val Pro Ala Lys Gln Ile Gly Thr Ser Glu Pro Ser
      100            105            110

Ser Pro Leu Ser Val Ala Ser Ser His Asp Asn Ser Cys Ser Asp Ser
      115            120            125

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Ser Ala Ala Ser Ile Phe Ser Asp Ser Lys Asn Asn Asn Ser Met Gln
 130 135 140

Met Leu Leu Thr Asp Asp Ile Glu Asp Ile Leu Glu Asp Ile Asp Asp
 145 150 155 160

Ala Glu Ile Tyr Asp Ala Glu Lys Val Thr Ile Thr Tyr Ile Ser Ser
 165 170 175

Lys Ser Cys

<210> 91

<211> 2154

<212> DNA

<213> Candida albicans

<400> 91

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cgtttagtat ttgaagatga acggaacgag tttgagcaat tgcaaagcga gtttgggtcag 1680
agaaagaagg atttgtacga gaaattgcgt cgctcgtcagc tagaggcatc tttgagtgat 1740

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agttttgaag ctgatagcga aaatgacgat gaatctgagc tcgccc aaat tcaacaagac 1800
 tttgaatcaa gcgccaacgc actcaagaca aagtttgaag cgaaaagaaa ggacctcata 1860
 aaccacgac cacctccaca gccaatgag acaccacagt tggatcttaa caacaagttt 1920
 agcttaccaa cagtgtatcc agagattatt cgaaacttgc cattagagtt gcgagggatt 1980
 gtccaagaaa gcaaggagga gcttccgcct atcaaaaagc ccataactcta tgtaactaca 2040
 taccctgaac gtccaaatcc agagtatctt acacgaatcg agattatcaa attgccaaat 2100
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<210> 92

<211> 717

<212> PRT

<213> *Candida albicans*

<400> 92

Met Ser Ile Thr Val Thr Phe Pro Lys Ser Pro Ser Thr Lys Lys Arg
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Ala Pro Ala Phe Gly Ile Glu Leu Glu Phe Ser Gln Gln Gly Ser Ser
 20 25 30

Asp Gly Ala Ile Glu Lys Ala Ala Leu Ala Val Pro Val Phe Ser Val
 35 40 45

Asp Asn Gln Asp Phe Val Leu Ile Arg Asp Leu Ala Lys Tyr Trp Gly
 50 55 60

Tyr Pro Ser Ser Tyr Gln Leu Ile Val Lys Leu Val Lys Cys Ala Asn
 65 70 75 80

Ile Glu Lys Ser Gln Ile Leu Lys Thr Asp Lys Asp Leu Asn Lys Glu
 85 90 95

Leu Phe Glu Leu Asp Leu Ile Glu Glu Ala Asp Thr Lys Ile Asp Leu
 100 105 110

Phe Tyr Ile Ser Leu Pro Leu Val Tyr Ser Arg Ile Glu Asn Lys Lys
 115 120 125

Val Phe Tyr Val Ser Arg Glu Pro Glu Gln Pro Lys Val Ser Lys Ala
 130 135 140

Pro Thr Gln Glu Lys Pro Ala Ser Val Val Ala Ala Glu Glu Asp Asp
 145 150 155 160

Asp Asn Leu Asp Asp Asp Glu Glu Asp Glu Val Asp Glu Asp Met Asp
 165 170 175

Glu Asp Asn Asp Asn Ser Gly Glu Leu Ser Lys Gly Tyr Lys His Met

180	185	190
His Lys Asp His Pro Lys Tyr Ile Asn Asp Asp Arg Val Thr Ile Gly		
195	200	205
Gln Val Phe His Gln Tyr Gly Leu Asp Pro Ser Thr Pro Leu Thr His		
210	215	220
Ser Leu Phe Asn Ser Ile Asn Ser Met Ser Lys Leu Asn Tyr Tyr Lys		
225	230	235 240
Asn Phe Gly Val Ser Gly Tyr Arg Phe Leu Pro Asn Ser Lys Leu Ser		
245	250	255
Tyr Ala Glu Arg Glu Leu Val Leu Asn Ala Asn Asn Tyr Asn Asp Met		
260	265	270
His Ile Asn Glu Lys Thr Glu Ser Lys Pro Lys Lys Ser Phe Arg Lys		
275	280	285
Pro Ile Gly Lys Ser Lys Lys His Asn Leu Gln Ile Asp Pro Asn Ser		
290	295	300
Ile Asp Leu Ser Glu Ser Val Ile Pro Gly Gln Gly Phe Ile Pro Asp		
305	310	315 320
Phe Ser Ile His His Leu Cys Lys Val Pro Asn Tyr Tyr Val Thr Ser		
325	330	335
Asn His Gln Ser Leu Pro Ser Ser Phe Asn Thr Lys Asn Leu Asn Ala		
340	345	350
Thr Ser Asn Ser Ser Tyr Leu Phe Asn Asp Asn Val Lys Ile Lys Ser		
355	360	365
Lys Ser Ile Gln Lys Leu Val Phe Asn Ser Asp Thr Asp Asn Tyr His		
370	375	380
His Thr Lys Tyr Phe Tyr Thr Lys Thr Tyr Arg Gly Pro Gly Ser Gly		
385	390	395 400
Asn Tyr Lys Asp Gly Ala Leu Met Asn Lys Ile Asn Lys Ile His Leu		
405	410	415
Ser Ser Asn Lys Lys Pro Arg His Lys Arg Lys Val Ser Asn Asn Asn		
420	425	430
Arg Tyr Asn Lys Ser Leu Lys Gly Leu Val His Glu Lys Phe Asp Lys		

435 440 445
 Asn Phe Val Glu Tyr Leu Leu Ser Glu Gln Arg Lys Tyr Thr Glu Asp
 450 455 460
 Tyr Ser Asn Leu Glu Ile Leu His Asn Ser Leu Gln Phe Asn Val Leu
 465 470 475 480
 Leu Asn Thr Tyr Arg Gly Val Ala Gln Glu Thr Trp Asn Asn Tyr Tyr
 485 490 495
 Lys Phe Lys Leu Ile Asp Phe Glu Gln Leu Lys Ala Leu Gln Met Glu
 500 505 510
 Ala Asn Glu Leu Glu Glu Arg Lys Leu Asp Ala Ala Arg His Gln Gln
 515 520 525
 Trp Ala Glu Glu Glu Lys Leu Arg Gln Glu Arg Leu Arg Leu Val Phe
 530 535 540
 Glu Asp Glu Arg Asn Glu Phe Glu Gln Leu Gln Ser Glu Phe Gly Gln
 545 550 555 560
 Arg Lys Lys Asp Leu Tyr Glu Lys Leu Arg Arg Arg Gln Leu Glu Ala
 565 570 575
 Ser Leu Ser Asp Ser Phe Glu Ala Asp Ser Glu Asn Asp Asp Glu Ser
 580 585 590
 Glu Leu Ala Gln Ile Gln Gln Asp Phe Glu Ser Ser Ala Asn Ala Leu
 595 600 605
 Lys Thr Lys Phe Glu Ala Lys Arg Lys Asp Leu Ile Asn Pro Ala Pro
 610 615 620
 Pro Pro Gln Pro Ile Glu Thr Pro Gln Leu Asp Leu Asn Asn Lys Phe
 625 630 635 640
 Ser Leu Pro Thr Val Tyr Pro Glu Ile Ile Arg Asn Leu Pro Leu Glu
 645 650 655
 Leu Arg Gly Ile Val Gln Glu Ser Lys Glu Glu Leu Pro Pro Ile Lys
 660 665 670
 Lys Pro Ile Leu Tyr Val Thr Thr Tyr Pro Glu Arg Pro Asn Pro Glu
 675 680 685
 Tyr Leu Thr Arg Ile Glu Ile Ile Lys Leu Pro Asn Ala Asn Ser Val

690

695

700

Gly Trp Asp Asn Phe Lys Lys Tyr Lys Asp Ser Asp Val
 705 710 715

<210> 93

<211> 411

<212> DNA

<213> Candida albicans

<400> 93

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 ggggaattac aagttaaatt aggagataaa ttctttccca tttcaagatt tgctaaacct 180
 catgctgttg ttcaccctgc tgatcaccat tcgaaagttg atgccaacaa gttccccgat 240
 gttgaaccag aacaaaaaca aaaagaggat ttaaaagagt ttaaccaaca agtcttaaag 300
 cctgacatta ataaaccaa ggttgatcct aattcatttc cagatattga accagaggct 360
 aaagaaagag aagccaaatt aaaagctgaa agacttaaaa agagccaata a 411

<210> 94

<211> 136

<212> PRT

<213> Candida albicans

<400> 94

Met Asn Arg Phe Leu Phe Asn Cys Leu Leu Phe Ile Gly Leu Leu Leu
 1 5 10 15

Ile Tyr Lys Tyr Leu Phe Met Ser Ala Asp Gly Lys Lys Glu Asp Ile
 20 25 30

Leu Glu Thr Gly Glu Lys Ile Asp Gly Glu Leu Gln Val Lys Leu Gly
 35 40 45

Asp Lys Phe Phe Pro Ile Ser Arg Phe Ala Lys Pro His Ala Val Val
 50 55 60

His Pro Ala Asp His His Ser Lys Val Asp Ala Asn Lys Phe Pro Asp
 65 70 75 80

Val Glu Pro Glu Gln Lys Gln Lys Glu Asp Leu Lys Glu Phe Asn Gln
 85 90 95

Gln Val Leu Lys Pro Asp Ile Asn Lys Pro Lys Val Asp Pro Asn Ser
 100 105 110

Phe Pro Asp Ile Glu Pro Glu Ala Lys Glu Arg Glu Ala Lys Leu Lys

115

120

125

Ala Glu Arg Leu Lys Lys Ser Gln
130 135

<210> 95

<211> 1193

<212> DNA

<213> Candida albicans

<400> 95

tgacataaaa cgtgtaacca ctacccaaaa gtgtatgttt aaaatactgt ataaacaaaa 60
ccaccctatt ctctgaacat tgaatcaact ttaagtttac tgttgataaa ttaagcaaaa 120
actttgcttc aaattcatat taaaatttta aaaacaattg atccatccat atttctttgc 180
tgccagccat cttctttttc tggttaagtc ttacacgact caagtgtgta aagttttttt 240
tttttgctac acgtcttgaa ttttttttcc ttccagaaat tttatatatt gaagccaatt 300
tcatttcgaa cttaatcatt tttttttata aatatttagc aaaataatta gccatatcaa 360
ttacaaataa tttttacatt tgaataaacc cagataaact ttcaaatacca tcctagcacc 420
ttcataatcc attctatata tttgcttctt tattgtctac agtcatttcc gttgcaatgt 480
cctcttctaa tgatacacca tctttatttg tcacaccaca aacaccacca agacagcaac 540
aaaggagaaa aagtaataca ggagctatat ctacaccagt tgccatca gttattattaa 600
ctccatctac aacaacaaaa aaacctacaa gaactccagt atcacagaaa agaaaacaag 660
gtgtacagtt gtctccacca caggcaaaaca aattccccct tactccaatc acccctcaaa 720
aatcaccatg caagacaaga aagaatttgg atttattcac tagtaacgaa aaatttggct 780
tattgttacc atcgccatcc actattgggt ctggtagatg tcataactct ttcacgcaag 840
ctccacctcc attatttgat ttgaagaagg ttaatgagtt taaagtacct aagacacccg 900
caaaacaaat tatagacaac tctagaacaa aagaatcaga aaatgaagat gactgggaag 960
tgatggacat agatgaagtt gccaaaattc ctctgcaaaa gttgaggaac ctttttatag 1020
acacttttga accaacgagt ccggttacac ctgaggagag tactggagat agaattaact 1080
atgacacaca tatggaattg ataaacagta aaactggtaa gaaaagagtt gtaaagttaa 1140
caaagaatca aatgaaaatc aaaccaaaga gattatcggt tgataatata taa 1193

<210> 96

<211> 238

<212> PRT

<213> Candida albicans

<400> 96

Met Ser Ser Ser Asn Asp Thr Pro Ser Leu Phe Val Thr Pro Gln Thr
1 5 10 15

Pro Pro Arg Gln Gln Gln Arg Arg Lys Ser Asn Thr Gly Ala Ile Ser
20 25 30

Thr Pro Val Ala Ser Ser Val Leu Leu Thr Pro Ser Thr Thr Thr Lys
35 40 45

Lys Pro Thr Arg Thr Pro Val Ser Gln Lys Arg Lys Gln Gly Val Gln
 50 55 60
 Leu Ser Pro Pro Gln Ala Asn Lys Phe Pro Phe Thr Pro Ile Thr Pro
 65 70 75 80
 Gln Lys Ser Pro Cys Lys Thr Arg Lys Asn Leu Asp Leu Phe Thr Ser
 85 90 95
 Asn Glu Lys Phe Gly Leu Leu Leu Pro Ser Pro Ser Thr Ile Gly Ser
 100 105 110
 Gly Arg Cys His Asn Ser Phe Thr Gln Ala Pro Pro Pro Leu Phe Asp
 115 120 125
 Leu Lys Lys Val Asn Glu Phe Lys Val Pro Lys Thr Pro Ala Lys Gln
 130 135 140
 Ile Ile Asp Asn Ser Arg Thr Lys Glu Ser Glu Asn Glu Asp Asp Trp
 145 150 155 160
 Glu Val Met Asp Ile Asp Glu Val Ala Lys Ile Pro Arg Ala Lys Leu
 165 170 175
 Arg Asn Pro Phe Ile Asp Thr Phe Glu Pro Thr Ser Pro Val Thr Pro
 180 185 190
 Glu Glu Ser Thr Gly Asp Arg Ile Asn Tyr Asp Thr His Met Glu Leu
 195 200 205
 Ile Asn Ser Lys Thr Gly Lys Lys Arg Val Val Lys Leu Thr Lys Asn
 210 215 220
 Gln Met Lys Ile Lys Pro Lys Arg Leu Ser Phe Asp Asn Ile
 225 230 235

 <210> 97
 <211> 888
 <212> DNA
 <213> Candida albicans

 <400> 97
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 aacaaatgct acgaaactga agttaccact ggtgttacca ccgtcactga agttgacact 180
 acgtacacca cctactgccc attgtcaacc actgaagctc cagctccatc tactgctact 240
 gatgtttcta ccaccgttgt caccatcacc tcatgtgaag aagacaaatg tcacgaaacc 300

gctgtcacca ccggtgtcac cactgtcact gaaggtacta ccactctacac tacctactgc 360
 ccattgccat ctactgaagc tccaggtcca gctccatcta ctgctgaaga atctaaacca 420
 gctgaatctt cccagttcc aaccaccgct gctgaatctt cccagctaa aactactgct 480
 gctgaatctt cccagctca agaaaccact ccaaagaccg ttgctgctga atcttcttca 540
 gctgaaacta ctgctccagc tgtctctacc gctgaagccg gtgctgctgc taacgctgtc 600
 ccagttgctg ctggtttgtt ggctttggct gctttgtttt aagtttacta gagcttaaata 660
 caaatattta caaacaaaat tttcattttc ccccttttcc ctttcttcat tcttcaaaaa 720
 aagggttatt tactattaat tgataaattt atggtttcat gttaatgtac cctttttttt 780
 ataaacattg ttattattat tatcatcatt agtttattta tattttcgtg aggttttccg 840
 gttaattaa attttttgga tacatattaa aaatttattt ggtactag 888

<210> 98

<211> 213

<212> PRT

<213> *Candida albicans*

<400> 98

Met Gln Phe Ser Ser Ala Val Val Leu Ser Ala Val Ala Gly Ser Ala
 1 5 10 15
 Leu Ala Ala Tyr Ser Asn Ser Thr Val Thr Asp Ile Gln Thr Thr Val
 20 25 30
 Val Thr Ile Thr Ser Cys Glu Glu Asn Lys Cys His Glu Thr Glu Val
 35 40 45
 Thr Thr Gly Val Thr Thr Val Thr Glu Val Asp Thr Thr Tyr Thr Thr
 50 55 60
 Tyr Cys Pro Leu Ser Thr Thr Glu Ala Pro Ala Pro Ser Thr Ala Thr
 65 70 75 80
 Asp Val Ser Thr Thr Val Val Thr Ile Thr Ser Cys Glu Glu Asp Lys
 85 90 95
 Cys His Glu Thr Ala Val Thr Thr Gly Val Thr Thr Val Thr Glu Gly
 100 105 110
 Thr Thr Ile Tyr Thr Thr Tyr Cys Pro Leu Pro Ser Thr Glu Ala Pro
 115 120 125
 Gly Pro Ala Pro Ser Thr Ala Glu Glu Ser Lys Pro Ala Glu Ser Ser
 130 135 140
 Pro Val Pro Thr Thr Ala Ala Glu Ser Ser Pro Ala Lys Thr Thr Ala
 145 150 155 160
 Ala Glu Ser Ser Pro Ala Gln Glu Thr Thr Pro Lys Thr Val Ala Ala

[illegible]

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<210> 99
<211> 977
<212> DNA
<213> Candida albicans
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[illegible]

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<210> 100
<211> 129
<212> PRT
<213> Candida albicans
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<400> 100
Met Ser Lys Asp Glu Tyr Phe Gly Lys Pro Ser Gly Pro Pro Pro Asn
  1             5             10             15
Tyr Asn Asn Gln Pro Gln Ser Gln Gln Pro Gln Gln Ser Tyr Val Pro
      20             25             30

```

Gln Ser Gln Pro Asn Tyr Ser Gln Gln Thr Gln Asp Arg Gly Met Phe
 35 40 45

Ser Gly Gly Gly Gly Gly His Gly His Tyr Gln Gln Gln Gln Gly Tyr
 50 55 60

Asn Ala Tyr Gly Pro Pro Pro Pro Gln Gly Gly Tyr Tyr Gln Gln Gln
 65 70 75 80

Pro Gly Gly Gly Gly Gly Tyr Tyr Gln Gln Gln Gln Gln Gln Pro
 85 90 95

Met Tyr Val Gln Gln Gln Pro Arg Ser Gly Gly Asn Asp Ser Cys Leu
 100 105 110

Met Gly Cys Leu Ala Ala Leu Cys Val Cys Cys Thr Leu Asp Met Leu
 115 120 125

Phe

<210> 101

<211> 2994

<212> DNA

<213> Candida albicans

<400> 101

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 accgataatg gatcaccaac cccacaagct gaaaaatcat tgaaaacatt aattgattta 120
 ttatacgata aagggtttgc cgcccaaatt agacctgggtg atttagacca tttgttagtc 180
 tttgttaaatt tgtcttcata caagttttct gaagaagctg aaaaagattt aattaaaaat 240
 tatgaatttg gtgtcacggg taaagatgac gtgttagctt ctaaacttag aattatttat 300
 caatacttaa cttatccaca atcagttggt ggatgtggta ttactcctaa ttctggggat 360
 tggaaatttg tcaccagtat tgttccaatt actaatgcct ttaatgaaac cacttttagtt 420
 gaagatttaa aaattaatgt tactcaacca aatttatcaa ttgccactat caaaaagaca 480
 tatggagttg aagttgctct ttattttgaa tatataaaac attacacttt ttgggttatta 540
 ttgctttcta ttattggtct tgtatctcat tttagaaaag ataaacgatt cctgttaact 600
 tttgccttta tcaatttgct ttgggggggtt ttattccttg catcatggca tagaagagaa 660
 caacatttgg ttaatgtatg ggggtgttcaa aatagtcatt taattgaaga acataattcc 720
 gaattggcta aagtcaatga aagatatgaa gaaaaatcaa cttatttcca tgcaataaat 780
 accaatggat tcagattttt aaaacaattg gcatttatcc ccattgcctt ggtgtttgtt 840
 ggtgttttga ttagttatca attgagttgt ttctgtattg aaatcttttt aaccgatatt 900
 tatgatggcc cggggaaatc tttattgact ttattaccaa cgggttttaac cagtgtattt 960
 gtgccaatth tgaccattgt ttataatgct gtcacggata ttattattaa atgggaaaaat 1020
 catgataacc aatatagcaa aaataattct attcttggtta aaacctttgt gttgaatttc 1080
 ttgactgggt atgttcatt aatcatcact tcattcatat atttaccatt tgctcatttg 1140
 gtgcaacctc atttaggtga tattaaaacc actattgccca catatgctgg tgaaaataga 1200

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ttctacacca aatacttggt gaaattaaag agtcaagaag aattttaaatt caatcaaggt 1260
agattagatg ctcaattctt ttatttcatt gtcacaaatc aagttatata attggtattg 1320
aaatatattc tccattggg ttaagattt gtatttaatt ttattgaaac gaaaattcag 1380
aagaaaacctc aattacaaac taaagatgat aacctgatg aatctatttg gttacataat 1440
gtcagattat cggtgaaact tcctgaatat aatggtgatg atgatttttag aggattagtt 1500
ttacaatttg gatatttgat aatggttggt ccagtttggc cattggcacc attggtttgt 1560
attattttca atttaatttt tttcaagttg gataatttta aattattgaa tggtaaatat 1620
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tcctcagttt tcttggtttt attaatggtt gtttcagaac atggattttt gattttgagt 1860
tatcttttat ttgaattctc ttctttgttc aagagtcaag ttgaatggga aaatgatttt 1920
gttgataatg atattaaatt gagacatgat tattattctg ggaaagtaaa accaacttat 1980
aaagtccact cggatgagtt gtgggagaag tttacccac aatcaacttt gaatttcact 2040
gttcctaaac caaccgcaga aactgatgat aaagttgaaa aaattgcttc taccgaaggt 2100
gcttatctga cttctgcaga aaaatctact actactgcta cttctcgttc tgataagagt 2160
aaaattcttg ctgaaaagga agctattttg aaacaaaagg aagctgagtt ggccgaatta 2220
gaaaagaaaa agaccaaact aaatgatttt aaagatccaa ccgattctgt cattaaaacc 2280
aatcaagtg ccaatggtaa agctgtgtta agtacaattg acaataacaa acatgttagt 2340
gatattgatc cagatgccgc cgccgcagca actgcaacat ctactgctaa tgattctggt 2400
gcaaaaaaat caacatcaac atcaacatca gcagccacag atactactaa cactgccccca 2460
tctcattctg gtccaactcc tgtcacttct tctgaaaaat caaacaacaa caacaacagt 2520
aagccaagtg atagtaccaa atctacttta gcaaatgatg aaacaagaaa aacacttgat 2580
cctaaaggcg ttggaagcac tacaacagggt gataaagaca cagtttcatc agacaaagca 2640
tctctgccaa ttgaagataa agaaagttca ccatccctag ctggaagtgc aacatcaaca 2700
ccaagtggaa ctgataaaaa aacatctcct aaaaaattag ttaccaatgc tgtcaataaa 2760
gttgaaaata atgatgattt caaaaaattc attaatgagg ctgaaaagga agctaaaaaa 2820
tccaaatctg gattgaaaaa attatttaac aagaagtaga agttgtttta attgtttcga 2880
tataaattgt atgaattcca gtttttttat ttttatttta ttttatttta gtttagtttt 2940
gatttcattt ttgtttttgt ttaatttgca atacaatata atgtttattt tttta 2994

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<210> 102

<211> 952

<212> PRT

<213> Candida albicans

<400> 102

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Met Thr Leu Pro Ile Gln Asp Leu Glu Pro Asp Tyr Tyr Ile Ser Val
  1                      5                      10                      15

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Asn Tyr Pro Thr Thr Asp Asn Gly Ser Pro Thr Pro Gln Ala Glu Lys
      20                      25                      30

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Ser Leu Lys Thr Leu Ile Asp Leu Leu Tyr Asp Lys Gly Phe Ala Ala
      35                      40                      45

```

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Gln Ile Arg Pro Gly Asp Leu Asp His Leu Leu Val Phe Val Lys Leu
      50                      55                      60

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Ser Ser Tyr Lys Phe Ser Glu Glu Ala Glu Lys Asp Leu Ile Lys Asn
 65 70 75 80
 Tyr Glu Phe Gly Val Thr Gly Lys Asp Asp Val Leu Ala Ser Lys Leu
 85 90 95
 Arg Ile Ile Tyr Gln Tyr Leu Thr Tyr Pro Gln Ser Val Gly Gly Cys
 100 105 110
 Gly Ile Thr Pro Asn Ser Gly Asp Trp Lys Phe Val Thr Ser Ile Val
 115 120 125
 Pro Ile Thr Asn Ala Phe Asn Glu Thr Thr Leu Val Glu Asp Leu Lys
 130 135 140
 Ile Asn Val Thr Gln Pro Asn Leu Ser Ile Ala Thr Ile Lys Lys Thr
 145 150 155 160
 Tyr Gly Val Glu Val Ala Leu Tyr Phe Glu Tyr Ile Lys His Tyr Thr
 165 170 175
 Phe Trp Leu Leu Leu Leu Ser Ile Ile Gly Leu Val Ser His Phe Arg
 180 185 190
 Lys Asp Lys Arg Phe Ser Leu Thr Phe Ala Phe Ile Asn Leu Leu Trp
 195 200 205
 Gly Val Leu Phe Leu Ala Ser Trp His Arg Arg Glu Gln His Leu Val
 210 215 220
 Asn Val Trp Gly Val Gln Asn Ser His Leu Ile Glu Glu His Asn Ser
 225 230 235 240
 Glu Leu Ala Lys Val Asn Glu Arg Tyr Glu Glu Lys Ser Thr Tyr Phe
 245 250 255
 His Ala Asn Asn Thr Asn Gly Phe Arg Phe Leu Lys Gln Leu Ala Phe
 260 265 270
 Ile Pro Ile Ala Leu Val Phe Val Gly Val Leu Ile Ser Tyr Gln Leu
 275 280 285
 Ser Cys Phe Cys Ile Glu Ile Phe Leu Thr Asp Ile Tyr Asp Gly Pro
 290 295 300
 Gly Lys Ser Leu Leu Thr Leu Leu Pro Thr Val Leu Ile Ser Val Phe
 305 310 315 320

Val Pro Ile Leu Thr Ile Val Tyr Asn Ala Val Thr Asp Ile Ile Ile
 325 330 335
 Lys Trp Glu Asn His Asp Asn Gln Tyr Ser Lys Asn Asn Ser Ile Leu
 340 345 350
 Val Lys Thr Phe Val Leu Asn Phe Leu Thr Gly Tyr Val Pro Leu Ile
 355 360 365
 Ile Thr Ser Phe Ile Tyr Leu Pro Phe Ala His Leu Val Gln Pro His
 370 375 380
 Leu Gly Asp Ile Lys Thr Thr Ile Ala Thr Tyr Ala Gly Glu Asn Arg
 385 390 395 400
 Phe Tyr Thr Lys Tyr Leu Leu Lys Leu Lys Ser Gln Glu Glu Phe Lys
 405 410 415
 Ile Asn Gln Gly Arg Leu Asp Ala Gln Phe Phe Tyr Phe Ile Val Thr
 420 425 430
 Asn Gln Val Ile Gln Leu Val Leu Lys Tyr Ile Leu Pro Leu Gly Leu
 435 440 445
 Arg Phe Val Phe Asn Phe Ile Glu Thr Lys Ile Gln Lys Lys Pro Gln
 450 455 460
 Leu Gln Thr Lys Asp Asp Asn Pro Asp Glu Ser Ile Trp Leu His Asn
 465 470 475 480
 Val Arg Leu Ser Leu Lys Leu Pro Glu Tyr Asn Val Asp Asp Asp Phe
 485 490 495
 Arg Gly Leu Val Leu Gln Phe Gly Tyr Leu Ile Met Phe Gly Pro Val
 500 505 510
 Trp Pro Leu Ala Pro Leu Val Cys Ile Ile Phe Asn Leu Ile Phe Phe
 515 520 525
 Lys Leu Asp Asn Phe Lys Leu Leu Asn Gly Lys Tyr Phe Lys Pro Pro
 530 535 540
 Val Pro Arg Arg Val Asp Ser Ile His Pro Trp Asn Leu Ala Leu Phe
 545 550 555 560
 Leu Leu Ala Trp Ile Gly Ser Ile Ile Ser Pro Val Val Thr Ala Phe
 565 570 575

Tyr Arg His Gly Thr Ala Pro Pro Lys Ser Met Gly Gln Phe Ala Leu
 580 585 590

Asp Lys Ala Ser Val His Val Ser Ser Ser Val Phe Leu Val Leu Leu
 595 600 605

Met Phe Val Ser Glu His Gly Phe Leu Ile Leu Ser Tyr Leu Leu Phe
 610 615 620

Glu Phe Ser Ser Leu Phe Lys Ser Gln Val Glu Trp Glu Asn Asp Phe
 625 630 635 640

Val Asp Asn Asp Ile Lys Leu Arg His Asp Tyr Tyr Ser Gly Lys Val
 645 650 655

Lys Pro Thr Tyr Lys Val His Ser Asp Glu Leu Trp Glu Lys Phe Thr
 660 665 670

Pro Gln Ser Thr Leu Asn Phe Thr Val Pro Lys Pro Thr Ala Glu Thr
 675 680 685

Asp Asp Lys Val Glu Lys Ile Ala Ser Thr Glu Gly Ala Tyr Ser Thr
 690 695 700

Ser Ala Glu Lys Ser Thr Thr Thr Ala Thr Ser Arg Ser Asp Lys Ser
 705 710 715 720

Lys Ile Leu Ala Glu Lys Glu Ala Ile Leu Lys Gln Lys Glu Ala Glu
 725 730 735

Leu Ala Glu Leu Glu Lys Lys Lys Thr Lys Leu Asn Asp Phe Lys Asp
 740 745 750

Pro Thr Asp Ser Val Ile Lys Thr Lys Ser Ser Ala Asn Gly Lys Ala
 755 760 765

Val Leu Ser Thr Ile Asp Asn Asn Lys His Val Ser Asp Ile Asp Pro
 770 775 780

Asp Ala Ala Ala Ala Ala Thr Ala Thr Ser Thr Ala Asn Asp Ser Gly
 785 790 795 800

Ala Lys Lys Ser Thr Ser Thr Ser Thr Ser Ala Ala Thr Asp Thr Thr
 805 810 815

Asn Thr Ala Pro Ser His Ser Gly Pro Thr Pro Val Thr Ser Ser Glu
 820 825 830

Lys Ser Asn Asn Asn Asn Asn Ser Lys Pro Ser Asp Ser Thr Lys Ser
 835 840 845
 Thr Leu Ala Asn Asp Glu Thr Arg Lys Thr Leu Asp Pro Lys Gly Val
 850 855 860
 Gly Ser Thr Thr Thr Gly Asp Lys Asp Thr Val Ser Ser Asp Lys Ala
 865 870 875 880
 Ser Ser Pro Ile Glu Asp Lys Glu Ser Ser Pro Ser Leu Ala Gly Ser
 885 890 895
 Ser Thr Ser Thr Pro Ser Gly Thr Asp Lys Lys Thr Ser Pro Lys Lys
 900 905 910
 Leu Val Thr Asn Ala Val Asn Lys Val Glu Asn Asn Asp Asp Phe Lys
 915 920 925
 Lys Phe Ile Asn Glu Ala Glu Lys Glu Ala Lys Lys Ser Lys Ser Gly
 930 935 940
 Leu Lys Lys Leu Phe Asn Lys Lys
 945 950

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 <212> PRT
 <213> Candida albicans

 <400> 103
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 Gln Gln Pro Gln Ile Leu Leu Thr Ser Pro His Leu Ile Ser Val Gln
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 Leu Ser Ser Leu Leu Ser Lys Asn Gln Thr Thr Thr Thr Val Ser
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<210> 104

<211> 4809

<212> DNA

<213> *Candida albicans*

<400> 104

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4809

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<211> 1603

<212> PRT

<213> Candida albicans

<400> 105

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Lys Val Phe Asp Phe Ser Val Thr Tyr Lys Leu Ala Arg Lys His Phe
 35 40 45

Glu Thr Ser Val Ala Leu Leu Lys Ala Phe Thr Leu Ser Glu Tyr Ala
 50 55 60

Ser Glu Tyr Ile Glu Asp Phe Asp Lys Val Thr Glu Val Gln Val Ser
 65 70 75 80

Glu Ser Glu Ile Ser Asp Leu Ser Ser Ile Asn Ser Ala Glu Ser Ile
 85 90 95

Pro Leu Asn Asp Ala Ser Pro Ser Glu Leu Asp Glu Ser Asn Thr Lys
 100 105 110

Lys Ile Lys Thr Val Leu Thr Val Arg Asp Ile Leu Val Ser Asn Ala
 115 120 125

Gly Lys Ser Asp Glu Lys Asp Pro Asp Arg Leu Thr Leu Ser Ile Pro
 130 135 140

Glu Val Asp Gly Arg Val Asp Met Phe Leu Val Trp Cys Cys Phe Tyr
 145 150 155 160

Ala Lys Thr Met Leu Glu Arg Phe Lys Pro Thr Val Glu Ser Ser Cys
 165 170 175

Thr Lys Asn Gln Ile Lys Ile Ile Arg Gly Pro Arg Lys Lys Leu Lys
 180 185 190

Leu Asp Val His Leu Asp Ser Val Ala Leu Val Ile Arg Leu Pro Arg
 195 200 205

Lys Val Asp Val Met Ile Glu Ile Asp Arg Ala Arg Leu Lys Asn Ala
 210 215 220

Leu Val Leu Lys Ser Ala Asp Ile Val Asn Cys Arg Leu Tyr Val Val
 225 230 235 240

Asp Pro Ser Thr Lys Phe Trp Ala Arg Leu Leu Ile Ile Lys Glu Pro
 245 250 255

Lys Phe Ser Ile Asp Phe Thr Lys Ser Ile His Asp Ala Tyr Phe Gly
 260 265 270

Ile Ser Thr Arg Ser Ile Arg Ile Ser Val Pro Asn Arg Phe Leu Phe
 275 280 285
 Tyr Thr Val Ile Asp Asn Phe Ile Thr Phe Phe Lys Ala Ile Lys Gln
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 Leu Ser Gln Asn Phe Arg Tyr Phe Asn Trp Gly Ile Asp Glu Phe Glu
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 Thr Ile Tyr Pro Ser Gln Lys Asn Ala Ile Val Phe Pro His Val Asn
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 Asn Lys Leu Ala Leu Ile Phe Glu Leu Gly Lys Ile Glu Gln Lys Glu
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 Arg Ile Arg Lys Trp Lys Ala Phe Glu Lys Lys Ser Gln Glu Ile Leu
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 Ser Thr Met Thr Pro Asn Val Ala Gly Asp Ser Ile Thr Arg Pro Asp
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 Phe Glu Glu Thr Lys Cys Arg Lys Trp Lys Glu Arg Gly Glu Asn Ile
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Trp Gly Ser His Asp Ile Asn Glu Val Met Lys Glu Lys Tyr Asp Ile
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Val Glu Tyr Asp His Gly Lys Pro Leu Thr Gly Ala Ile Phe Arg Asp
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Val Asp Leu Thr Leu Asp Lys Phe Lys Leu Gly Asp Val Asp Lys Phe
 565 570 575

Leu Tyr Asp Tyr Ala Lys His Gln Pro Lys Leu Thr Tyr Ser Ile Leu
 580 585 590

Cys Pro Met Tyr Val Glu Leu Lys Ala Arg Lys Phe Tyr Met Ile Leu
 595 600 605

Lys Asp Tyr Pro Leu Pro Val Ala Ser Phe Pro Arg Ser Asn Thr Pro
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Ser Ser Pro Thr Ile His Ile Lys Thr Asn Leu Val Ile His Glu Lys
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Leu Phe Ser Arg Lys Glu Glu Leu Arg Tyr Ile Tyr Val Pro Phe Ser
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Pro Ala Val Pro Asp Asp Gly Arg Ala Asp Asn Phe Tyr Ser Val Asn
 660 665 670

Ile Pro Arg Thr Leu Thr Pro Val Lys Val Ala Ala Asp Phe Asn Cys
 675 680 685

Asp Leu Asn Thr Asp Arg Ser Cys Thr Ile Ser Trp Cys Lys Ser Tyr
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Pro Ala Ile Asp Asp Ser Pro Ile Gly Trp Trp Asp Lys Ile Pro Leu
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Ile Val His Gly Arg Tyr Gln Phe Asn Ile Ala Asn Glu Leu Cys Leu
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His Met Lys Ser Gly Arg Asn Pro His Glu Leu Ile Gly Lys Asn Ala
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Gly Phe Val Phe Cys Trp Lys Asn Asn Val Lys Leu Val Ile Asp Gly
 770 775 780

Thr Ile Asn Ser Lys Asp Leu Val Val Leu Glu Ser Asp Asp Phe Ile
 785 790 795 800
 Phe Ala Ile Pro Asn Tyr Ser Ile Glu Glu Lys Asn Val Trp Ser Leu
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 Phe Tyr Asp Asp Phe Asp Asp Pro Val Pro Asp Ile Glu Leu Glu Ser
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 Lys Lys Phe Asn Lys Tyr Val Ile Lys Leu Ser Ser Ser Glu Arg Val
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 Arg Trp Val Leu Gly Met Leu Phe Glu Arg Asn Lys Tyr Pro Thr Gln
 850 855 860
 Lys Phe Ser Asp Glu Glu Leu Arg Val Ser Thr Phe Lys Pro His Tyr
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 Glu Val Met Ile Thr Asn Pro Ala Asn Glu Phe His Pro Asp Ser Tyr
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 Glu Gly Tyr Arg Ser Asp Tyr Val His Met Ser Leu Ser Val Ile Ser
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 Arg Ala Lys Thr Gly Glu Thr Ala Asn Thr Ala Tyr Phe Thr Pro Leu
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 Ser Phe His His Phe Phe Tyr Trp Trp Asp Thr Leu Leu His Tyr Ser
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 Pro Pro Pro Ile Lys Arg Gly Lys Leu Phe Glu Met Asp Gln Val Lys
 945 950 955 960
 Lys Pro Lys Ile Lys Phe Gly Thr His Met Phe Thr Met Lys Tyr Gln
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 Leu Ile Phe Asn Pro Val Thr Ile Ser His Leu Tyr Arg His Ser Thr
 980 985 990
 Ser Asp Val Pro Lys Lys Asn Ser Arg Val Ala Phe Thr Gly Leu Lys
 995 1000 1005
 Gly Arg Phe Asp Val Cys Glu Ile Asp Leu His Gln Arg Arg Glu Tyr
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 Val Thr His Glu Asn Lys Lys Leu Asn Arg Lys Thr Lys Ile Arg His
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Leu Lys Met Asn Gln Ala Glu Val Asn Ile Glu Asn Ala Asp Ala Arg
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 Val Ile Tyr Ala Leu Phe Asn Asp Thr Ser Val Thr Gly Lys Leu Met
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 Thr Tyr Leu Asn Ala Asp Ser Ser Asp Ser Ser Thr Asp Gly Ser Gln
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 Ser Ser Asp Tyr Arg Gly Ser Ser Tyr Ser Arg Trp Leu Glu Asn Val
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 Glu Ile Ser Asp Gly Asp Phe Ser Trp Tyr Asp Pro Lys Asp Phe Ile
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 Glu Leu Glu Val Arg Glu Pro Leu Ser Pro Tyr Pro Lys Thr Lys Ile
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 Ala Ile Ile Gln Lys Ser Pro Asn Gln Leu Phe Ile Ser Ser Glu Lys
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 Leu Glu Gln Gly Asn Glu Leu Val Val Tyr Leu Ser Lys Tyr Val Ile
 1540 1545 1550

Asn Ala Thr Ser Ala Gln Tyr Ser Ser Ile Tyr Tyr Val Ile Thr Gly
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Leu Leu Leu Ser Asn Asp Asp Lys Glu Ser Asn Tyr Asn Gly Arg Leu
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<211> 728

<212> DNA

<213> Candida albicans

<400> 106

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<210> 107

<211> 52

<212> PRT

<213> Candida albicans

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Glu Lys Asn Ile Phe Thr His Ser Leu Pro Leu Phe Phe Phe Thr
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Ile Ala Thr Asn

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<210> 108

<211> 440

<212> DNA

<213> Candida albicans

<400> 108

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440

<210> 109

<211> 55

<212> PRT

<213> Candida albicans

<400> 109

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Phe Lys Phe Lys Asp Trp Glu Thr Arg Val Phe Ser Tyr Cys Leu His
      20             25             30

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Phe Leu Lys Phe Asp Lys Arg Ile Val Ser Leu Cys Leu Ile Tyr Tyr
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Glu Met Ile Arg Ile Lys Lys
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<210> 110

<211> 481

<212> DNA

<213> Candida albicans

<400> 110

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<210> 111

<211> 126

<212> PRT

<213> Candida albicans

<400> 111

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Pro Lys Thr Cys Gly Leu Lys Lys Val Pro Ile Ser Gln Pro Gln Gln
 35 40 45

Pro Leu Gln Thr Pro Ser Phe Ala Gln His Ile Phe Ile Gly Ser Pro
 50 55 60

Thr Cys His Tyr Asn Leu Arg Ser Pro Ser Leu Ile Val Val Ala Pro
 65 70 75 80

His Ser Leu Lys Leu Thr Pro Asn Phe Ala Ile Phe Gln Lys Phe Ser
 85 90 95

Leu Phe Arg Val Val His Ala Gln Ile His Phe Phe Ser Ala Gly Pro
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Lys Asn Thr Arg Phe Phe Asn Pro Pro Glu Leu Asp Val Tyr
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<210> 112

<211> 259

<212> PRT

<213> Candida albicans

<400> 112

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35	40	45
Pro Lys Asp Arg Ile Leu Lys Thr His Gln Gly Tyr Gly Phe Val Glu		
50	55	60
Phe Lys Asn Ser Ala Asp Ala Lys Tyr Thr Met Glu Ile Leu Arg Gly		
65	70	75
		80
Ile Arg Leu Tyr Gly Lys Ala Leu Lys Leu Lys Arg Ile Asp Ala Lys		
85	90	95
Ser Gln Ser Ser Thr Asn Asn Pro Asn Asn Gln Thr Ile Gly Thr Phe		
100	105	110
Val Gln Ser Asp Leu Ile Asn Pro Asn Tyr Ile Asp Val Gly Ala Lys		
115	120	125
Leu Phe Ile Asn Asn Leu Asn Pro Leu Val Asp Glu Ser Phe Leu Met		
130	135	140
Asp Thr Phe Ser Lys Phe Gly Thr Leu Ile Arg Asn Pro Ile Ile Arg		
145	150	155
		160
Arg Asp Ser Glu Gly His Ser Leu Gly Tyr Gly Phe Leu Thr Tyr Asp		
165	170	175
Asp Phe Glu Ser Ser Asp Leu Cys Ile Gln Lys Met Asn Asn Thr Ile		
180	185	190
Leu Met Asn Asn Lys Ile Ala Ile Ser Tyr Ala Phe Lys Asp Ser Ser		
195	200	205
Val Asp Gly Lys Lys Ser Arg His Gly Asp Gln Val Glu Arg Lys Leu		
210	215	220
Ala Glu Ser Ala Lys Lys Asn Asn Leu Leu Val Thr Lys Thr Ser Lys		
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<213> *Candida albicans*

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2021

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<213> *Candida albicans*

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      35           40           45
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Gly Leu Ala Arg Val Thr Val Pro Gly Ser Asp Val Ser Lys Asn Ile
      65           70           75           80
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Pro Val Val Ala Lys Ser Ser Ser Ala Ser Lys Pro Ser Phe Val Pro
      165          170          175
Lys Ser Thr Gly Lys Pro Val Ala Pro Ala Lys Pro Lys Pro Lys Asn
      180          185          190
Ile Thr Lys Asp Ala Gly Trp Gly Asp Ala Glu Asp Val Glu Glu Arg
      195          200          205
Asp Phe Asp Lys Lys Pro Leu Asp Asn Val Pro Ser Ala Tyr Lys Pro
      210          215          220
Thr Lys Val Asn Ile Asp Glu Leu Arg Lys Gln Lys Ser Asp Thr Thr
      225          230          235          240
Ser Ser Thr Pro Lys Thr Phe Lys Ser Glu Pro Gln Glu Glu Lys Asn
      245          250          255
Asp Asp Asp Gly Gln Ser Lys Pro Leu Ser Glu Arg Met Lys Ala Tyr

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 Pro Lys Ala Glu Ala Glu Glu Ser Lys Lys Gln Ser Thr Thr Ala Thr
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Phe Ser Glu Gly Asp Leu Ile Val Glu Ile Glu Phe Val Asp Asp Asp		
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Trp Trp Gln Gly Lys His Ser Lys Thr Gly Glu Val Gly Leu Phe Pro		
625	630	635 640
Ala Asn Tyr Val Val Leu Asn Glu		
645		